

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:40:22 ; Search time 25 Seconds

(without alignments)
2484.207 Million cell updates/sec

Title: US-09-744-748-1

Perfect score: 1970

Sequence: 1 MTSTSGILRPLFLVCIILG.....HVKRHOYKSVGNLEKFWFN 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp Vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	100.0	359	11 O88819	O88819 mus musculus
2	1961	99.5	359	4 Q9Y231	Q9Y231 homo sapien
3	1956	99.3	359	11 Q9JIG1	Q9JIG1 cricetus
4	1955	99.2	359	11 Q99JB3	Q99JB3 rattus norv
5	908.5	46.1	391	13 Q9W640	Q9W640 brachydanio
6	839	42.6	392	13 Q9W641	Q9W641 gallus gall
7	791	40.2	356	13 Q98952	Q98952 rattus norv
8	704.5	35.8	433	11 Q99N88	Q99N88 rattus norv
9	696	35.3	362	11 Q9R220	Q9R220 cricetus
10	694	35.2	362	11 Q9R219	Q9R219 cricetus
11	693	35.2	401	11 Q9JIK2	Q9JIK2 cricetus
12	689	35.0	362	11 Q95886	Q95886 cricetus
13	688.5	34.9	386	11 Q920V9	Q920V9 mus musculus
14	688	34.9	390	11 Q920W0	Q920W0 mus musculus
15	687	34.9	390	11 Q920W1	Q920W1 mus musculus
16	687	34.9	390	11 Q920V7	Q920V7 mus musculus

17	687	34.9	390	11 Q91VB5	Q91VB5 mus musculus
18	687	34.9	390	11 Q91V20	Q91V20 mus musculus
19	686	34.8	390	11 Q920V6	Q920V6 mus spicile
20	683	34.7	390	11 Q920V8	Q920V8 mus musculus
21	672	34.1	360	6 Q9XT34	Q9XT34 sus scrofa
22	670	34.0	361	4 Q9PLW6	Q9PLW6 homo sapien
23	667.5	33.9	359	4 Q9UND8	Q9UND8 homo sapien
24	664.5	33.7	359	6 Q9GKU6	Q9GKU6 pongo pygma
25	657	33.4	365	6 Q9TQQ3	Q9TQQ3 bos taurus
26	582	29.5	351	5 Q76204	Q76204 schistosoma
27	387	19.6	426	5 Q9WJ24	Q9WJ24 schistosoma
28	314	15.9	400	5 Q01906	Q01906 caenorhabdi
29	304	15.4	1652	5 Q22202	Q22202 caenorhabdi
30	302	15.3	312	5 Q9NSH5	Q9NSH5 caenorhabdi
31	285.5	14.5	451	5 Q21362	Q21362 caenorhabdi
32	258	13.1	489	11 Q9CXS9	Q9CXS9 mus musculus
33	235.5	12.0	405	10 Q93X61	Q93X61 beta vulgar
34	222	11.3	268	10 Q93WR9	Q93WR9 medicago tr
35	201	10.2	219	10 Q93WS0	Q93WS0 medicago tr
36	197	10.0	510	10 Q9ST51	Q9ST51 phaseolus a
37	191.5	9.7	445	5 Q9W0F6	Q9W0F6 drosophila
38	170.5	8.7	292	5 Q76544	Q76544 dictyostell
39	157	8.0	475	2 Q918S4	Q918S4 helicobacte
40	156.5	7.9	183	16 Q92GR3	Q92GR3 rickettsia
41	156.5	7.9	338	2 Q87135	Q87135 vibrio chol
42	154.5	7.8	346	2 Q87156	Q87156 vibrio chol
43	153.5	7.8	338	2 Q34231	Q34231 vibrio chol
44	145	7.4	478	2 Q30511	Q30511 helicobacte
45	140.5	7.1	333	2 Q32631	Q32631 helicobacte

ALIGNMENTS

RESULT 1

ID	O88819	PRELIMINARY;	PRT;	359 AA.
AC	O88819;			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX) (MFUC-TIX).			
GN	FUT9.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.			
RC	STRAIN=BALB/C; TISSUE=BRAIN;			
RX	MEDLINE=98434588; PubMed=9756916;			
RA	Kudo T., Ikehara Y., Togayachi A., Kaneko M., Hiraga T., Sasaki K.,			
RA	Narimatsu H.;			
RT	"Expression cloning and characterization of a novel murine alpha1, 3-fucosyltransferase, mFuc-TIX, that synthesizes the Lewis x (CD15) epitope in brain and kidney."			
RL	J. Biol. Chem. 273:26729-26738(1998).			
CC	-!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF LEWIS X AND LEWIS Y.			
CC	-!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYLR = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR.			
CC	-!- PATHWAY: GLYCOSYLATION.			
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.			
CC	-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN AND KIDNEY. IT ALSO EXPRESSED IN THE STOMACH, COLON, UTERUS AND EPIDIDYMIS. NOT FOUND IN THYMUS, LIVER, SPLEEN, Ovary, LUNG, HEART, TESTIS AND SMALL INTESTINE.			
DR	EMBL: AB015426; BAA33522.1; -			
DR	MGI: MGI:1330859; Fut9.			
DR	InterPro: IPR001503; Glyco_transf_10.			

QW	Transferase; Glycosyltransferase.	99.5%;	Score 1961;	DB 4;	Length 359;
SQ	SEQUENCE 359 AA; 42041 MW; C90CF5C02CB644D9 CRC64;	Best Local Similarity 99.2%;	Pred. No. 5.5e-142;	Mismatches 2;	Indels 0; Gaps
		Matches 356;	Conservative		
QY	1 MTSKSGILRLPFLVICIILGCFMACLLIYIKPTNSWVFSPMESASSLVKMKNFESTKTDY 60				
Db	1 MTSKSGILRLPFLVICIILGCFMACLLIYIKPTNSWVFSPMESASSLVKMKNFESTKTDY 60				
QY	61 FNETTILVWVPFGOTDLTSCAMENIOGCHLTTRDSLYNKSHAVILHHRDLSWDLTNL 120				
Db	61 FNETTILVWVPFGOTDLTSCAMENIOGCHLTTRDSLYNKSHAVILHHRDLSWDLTNL 120				
QY	121 PQOARPPQKVIWNLESPTHTPKQSGIEHLNLTLYRRSDIOVPGYGLTVSTNPFV 180				
Db	121 PQOARPPQKVIWNLESPTHTPKQSGIEHLNLTLYRRSDIOVPGYGLTVSTNPFV 180				
QY	181 EYVPSKEKLVCVSNWNPENHARVYKYNELSKSIEHTYGOAFGEVYNDKNLIPTISTCKF 240				
Db	181 EYVPSKEKLVCVSNWNPENHARVYKYNELSKSIEHTYGOAFGEVYNDKNLIPTISTCKF 240				
QY	241 YLSFENS1HKDYITEKLYNAPLAGSVVVLGFSRNYENYIPADSF1HVEDFNSPSELAK 300				
Db	241 YLSFENS1HKDYITEKLYNAPLAGSVVVLGFSRNYENYIPADSF1HVEDFNSPSELAK 300				
QY	301 YLKEVDKNNKLYSYFNWRKDFTNVLPWFESHACIADHVYKRGQYKSYGNLEKFWFN 359				
Db	301 YLKEVDKNNKLYSYFNWRKDFTNVLPWFESHACIADHVYKRGQYKSYGNLEKFWFN 359				
RESULT 3					
Q9JIG1	PRELIMINARY; PRT: 359 AA.				
ID	Q9JIG1				
AC	Q9JIG1				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)				
DE	ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX).				
DE	FUT9.				
GN	Cricetulus griseus (Chinese hamster).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus				
OX	NCBI_Taxid=10029;				
OX	(1)				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=OVARY.				
RC	MEDLINE=2016953; PubMed=10700388;				
RC	Fatnakh S.K., Zhang A., Shi S., Stanley P.;				
RA	"Alpha(1,3)fucosyltransferases expressed by the gain-of-function Chinese hamster ovary glycosylation mutants LEC12, LEC29, and LEC30."				
RL	Arch. Biochem. Biophys. 375:322-332(2000).				
RL	-!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF LEWIS X AND LEWIS Y.				
CC	-!- CATALYTIC ACTIVITY: GDP-L-Fucose + 1,4-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.				
CC	-!- PATHWAY: GLYCOSYLATION.				
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.				
CC	EMBL; AF230460; AAF82412.1; -.				
DR	InterPro; IPR001503; Glyco_transf.10.				
DR	Pfam; PF00852; Glyco_transf.10; 1.				
KW	Transferase; Glycosyltransferase;				
DR	Signal-anchor; Golgi stack.				
FT	DOMAIN 1 11 CYTOPLASMIC (POTENTIAL),				
FT	TRANSMEM 12 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL),				
FT	DOMAIN 31 359 LUMENAL CATALYTIC (POTENTIAL).				
FT	CARBOHYD 52 62 UNLINKED GLYCANA (DOCTRYNAL).				

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FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 42071 MW; 9D5CD8BFF07EA902 CRC64;

Query Match 99.3%; Score 1956; DB 11; Length 359;
Best Local Similarity 98.9%; Pred. No. 1.3e-141;
Matches 355; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
DB 1 MTSTSGILRPFLIVCIIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
QY 61 FNETTILVWVWPGQFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
DB 61 FNETTILVWVWPGQFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
QY 121 PQOARPPQKWIWMNLESPHTPKSGIEHLENLTITRYRDSDIQVPGFLTIVSTNPFVF 180
DB 121 PQOARPPQKWIWMNLESPHTPKSGIEHLENLTITRYRDSDIQVPGFLTIVSTNPFVF 180
QY 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTISTCKF 240
DB 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTISTCKF 240
QY 241 YLSFENSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
DB 241 YLSFENSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
QY 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACIACDHVKRHOEYKSVGNLEKWFVN 359
DB 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACIACDHVKRHOEYKSVGNLEKWFVN 359

RESULT 4
Q99JB3 PRELIMINARY; PRT; 359 AA.
ID Q99JB3
AC Q99JB3
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE ALPHA(1.3)-FUCOSYLTRANSFERASE IX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimoda Y., Tajima Y., Osanai T., Katsume A., Kohara M., Kudo T.,
RA Narimatsu H., Osumi N., Sanai Y.;
RT "Expression of Lewis x epitope in embryonic forebrain by regulating
RT alpha(1,3)-fucosyltransferase IX expression.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=20472964; PubMed=11020213;
RA Baboval T., Henion T., Kinnally E., Smith F.I.;
RT "Molecular cloning of rat alpha(1,3)-fucosyltransferase IX and
RT comparison of the expression of fuc-TIV and fuc-TIX genes during rat
RT postnatal cerebellum development.";
RL J. Neurosci. Res. 62:206-215(2000).
[3]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Smith F.I., Baboval T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049819; BAB40953.1; -.
DR EMBL; AF345993; AAK16591.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 359 AA; 42037 MW; 369B4A7BD0C6CC80 CRC64;

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Query Match 99.2%; Score 1955; DB 11; Length 359;
Best Local Similarity 99.2%; Pred. No. 1.6e-141;
Matches 356; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLIVCIIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
DB 1 MTSTSGILRPFLIVCIIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
QY 61 FNETTILVWVWPGQFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
DB 61 FNETTILVWVWPGQFDLTSCQAMENIQGCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
QY 121 PQOARPPQKWIWMNLESPHTPKSGIEHLENLTITRYRDSDIQVPGFLTIVSTNPFVF 180
DB 121 PQOARPPQKWIWMNLESPHTPKSGIEHLENLTITRYRDSDIQVPGFLTIVSTNPFVF 180
QY 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTISTCKF 240
DB 181 EVPSKEKLVWVYNNPNHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTISTCKF 240
QY 241 YLSFENSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
DB 241 YLSFENSIHKDYITEKLYNAFLAGSPVVLGSPRENYENIPADSFTHVEDFNSPSELAK 300
QY 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACIACDHVKRHOEYKSVGNLEKWFVN 359
DB 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWEHSHACIACDHVKRHOEYKSVGNLEKWFVN 359

RESULT 5
Q9W640 PRELIMINARY; PRT; 391 AA.
ID Q9W640
AC Q9W640;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ALPHA(1.3)-FUCOSYLTRANSFERASE.
GN FTI OR ZFTI.
OS Brachydanio rerio (Zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kageyama N., Natsuka S., Hase S.;
RT "Molecular cloning and characterization of two zebrafish
RT alpha(1,3)-fucosyltransferase genes developmentally regulated in
RT embryogenesis.";
RL J. Biochem. 0:0-0(1999).
DR EMBL; AB023627; BAA76706.1; -.
DR ZFIN; ZDB-GENE-990715-17; ft1.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 391 AA; 45265 MW; 98826D0B3D9679C2 CRC64;

Query Match 46.1%; Score 908.5; DB 13; Length 391;
Best Local Similarity 45.5%; Pred. No. 1.4e-61;
Matches 178; Conservative 58; Mismatches 116; Indels 39; Gaps 6;

QY 1 MTSTSGILRPFLIVCIIILGCFMACLLIYIKPTNSWVSP-----MESASSVLKM 50
DB 6 LTPPSKA-AQKVIATFMLISFCIFPVYNNPTTFKFFPAVDVHTNCSTETCLDLVK 64
QY 51 KNFST-----KTDYFNETTILVWVWPGQFDLTSCQAMFNI 88
DB 65 QNYKCTIKNASDNPSTTAPNAPATAKDD--QETILLIWTYPFGAREDLGCGSQFNI 122
QY 89 QGCHLTTRDSLYNKSHAVLIHHRDISWDLTNLPQARPPQKWIWMNLESPHTPKSGI 148
DB 123 HGCHLTDRDSMIQKAGVWFHHRDLSDAD---LPQPPRPAFKQKWIWMNLESPSHNSLI 179

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QY 149 EHLNLTJYRRDSDIOVPYGFLLTVSNPFV-FEVPSKEKLVCMVSNWNNPEHARVYKN 207
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 180 NDNGLNSSFRRKSDIIPVYGRLLDAYDEQKNFTIPKDKLVCIWVSNFQEHKRQSYIN 239
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 208 ELKSIEIHTYGOAFGEYVNDKNLIPTISCKYLSFENSIRKDYITEKLYNAFLAGSVP 267
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 240 ELVHKIYVAYGHHNRRVNDYDGNVSSCKFYLSFENSIRHRYFTEKLFNPLALGTVP 299
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 268 VVLGSPRENYENYIPADSFTHVEDFNSPSELAKYLKVEVDKNNKLYLSYFNWRKDFVNLN 327
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 300 VVLGSPRDNVEEIPRDAFIHVDFFPKELADHLKSLDQNEQYRQYFNWRKHFTISMSS 359
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 328 RFWESHACLAGDVKHROEYKSVGNLSEKWF 358
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 360 SFGLEHACRTCDYLKRNKHYIAIKDLKGEWF 390
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 6
QY 641 PRELIMINARY: PRT; 392 AA.
AC Q9W641
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ALPHA(1,3)FUCOSYLTRANSFERASE.
GN FT2 OR ZFT2.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kageyama N., Natsuka S., Hase S.;
RT "Molecular cloning and characterization of two zebrafish
RT alpha(1,3)fucosyltransferase genes developmentally regulated in
RT embryogenesis.";
RL J. Biochem. 0:0-0(1999).
DR EMBL; AB023628; BAA76707.1; -.
DR ZFIN; ZDB-GENE-990715-18; ft2.
DR InterPro; IPR001503; Glyco.transf.10.
DR Pfam; PF00852; Glyco.transf.10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 392 AA; 45944 MW; ABAC437E549C6114 CRC64;

Query Match 42.6%; Score 839; DB 13; Length 392;
Best Local Similarity 42.8%; Pred. No. 2,8e-56;
Matches 164; Conservative 61; Mismatches 122; Indels 36; Gaps 7;

QY 3 STSGILRPFLIVCIIIGCFMACLL-IYKPTNSWFSP-----MESASSVLMK 51
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 18 STQKLIVTFMLISLV-----CIFVYVNPNTFTFYPMGTHANSSCETCLHVKMQ 71
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 52 NF-ESTTDYFN-----ETTILVWVPFGQTFDLTSCQAMFNIOGCHLT 96
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 72 NYECIMKASYNALPTPAPNPAKGDQDIIVLIWMAFPVDFDLKDCGLEYNHGCQLYD 131
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 97 RSLYNKSHAVLIHHRDISWDLTNLPQOARPPFKQKWIWNLSPHTHPQKSGIEHFNLT 156
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 132 RSLQKAGVNFHRDMS---TDFPQPRDPDFQKWIWNLSPHTHPQKSGIEHFNLT 188
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 157 TYRSDSDIQVPGELTVST-NPFVFEVPSKEKLVCMVSNWNNPEHARVYKNLSKSI 215
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 189 SYNDSIDIPVYGLVDATTEQKFTIPKDKLVCIWVSNFQEHKRQSYIN 248
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 216 HTYGOAFGEYVNDKNLIPTISCKYLSFENSIRKDYITEKLYNAFLAGSVPVNLN 275
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 249 STYGHHNRRINGDDYDGNVSSCKFYLSFENSIRHRYFTEKLFNPLALGTVPV 308
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 276 NYENYIPADSFTHVEDFNSPSELAKYLKVEVDKNNKLYLSYFNWRKDFVNLN 335
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 309 NYEFIPRDAFIHVDFFPKELADHLKSLDQNEQYRQYFNWRKHFTISMSS 368
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

```
QY 336 LACDVKHVRHROEYKSVGNLEKWF 358
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 369 RICDYLKRNKHYIAVTDLKGWF 391
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 7
QY 8952 PRELIMINARY: PRT; 356 AA.
AC Q98952
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ALPHA(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.73)
DE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
DE (CTF1).
GN CTF1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-97115837; PubMed-8955139;
RA Lee K.P., Carlson L.M., Woodcock J.B., Ramachandra N., Schultz T.L.,
RA Davis T.A., Lowe J.B., Thompson C.B., Larsen R.D.;
RL J. Biol. Chem. 271:32960-32967(1996).
CC -!- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.
CC -!- PATHWAY: GLYCOSYLATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -!- TISSUE SPECIFICITY: IN THE FOLLOWING EMBRYONIC TISSUES: BRAIN,
CC EYE, GIZZARD, THYMUS, BURSA AND SPLEEN.
CC EMBL; U73678; AAC60060.1; -.
DR InterPro; IPR001503; Glyco.transf.10.
DR Pfam; PF00852; Glyco.transf.10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 51 SIGNAL-ANCHOR
FT TYPE-II MEMBRANE PROTEIN.
FT LUMENAL, CATALYTIC (POTENTIAL).
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 356 AA; 41494 MW; 13141627FE8AD089 CRC64;

Query Match 40.2%; Score 791; DB 13; Length 356;
Best Local Similarity 50.3%; Pred. No. 1.2e-52;
Matches 151; Conservative 49; Mismatches 94; Indels 6; Gaps 5;

QY 63 ETTILVWVPFGQTFDLTSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDIS-WDLTNLP 121
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 56 EYTVLLWPEFGFRWRPADCRRRYNTGCLISADRGYGEARAVLFHHRDLALHGRQLP 115
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 122 Q--QARPPFQKWIWNLSPHTHPQKSGIEHFNLTLYRRDSDIQVPGELTVSTNPFV 179
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 116 RGPFPFRPRQRVWVNNFSPSHSGPLRGLAGLFNNMTSYRRDSOVFPYGYLYEPSPRP 175
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 180 FVPSKEKLVCMVSNWNNPEHARVYKNLSKSIETHTYGOAFGEYVNDKNLIPTISCK 239
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 176 FVLPRKSLVAVVISNNEEHARVYRQLKEHLPIDVYG-ARGMALLEGSVKTVTSAYK 234
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 240 FYLSFENSIRHRYFTEKLYNAFLAGSVPVNLNPREWESHACLDHVK-RHOEYKSVGNLEKWF 298
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 235 FYLAFENSQHTDYITEKLVNAFAASAVPVVLGPRRNYERFIPADSFTHVDFFSPRL 294
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 299 AKYLEVDKNNKLYSYFNWRKDFVNLNPREWESHACLDHVK-RHOEYKSVGNLEKWF 357
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 295 ATYLAFLDKNKPYSRRYFAWRNKYEHVTSFWEHYCKVCEAVRTAGNQLTVQNLAGWF 354
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```



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RESULT 8
Q99N88 PRELIMINARY; PRT; 433 AA.
AC Q99N88;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE ALPHA1,3-FUCOSYLTRANSFERASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanai Y., Shimoda Y., Tajima Y., Otsu T., Katsume A., Kohara M.,
RA Kudo T., Narimatsu H., Osumi N.;
RT "Expression of Lewis x epitope in embryonic forebrain.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049938; BAB40992.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 433 AA; 48918 MW; 1E1AFFB70EFA1402 CRC64;

Query Match 35.8%; Score 704.5; DB 11; Length 433;
Best Local Similarity 39.6%; Pred. No. 6e-46;
Matches 160; Conservative 51; Mismatches 118; Indels 75; Gaps 13;

QY 4 TSKGILRPFLVCIILGCFMACLLIYIKPTNSWVFSPMESASSVLKMKNFSTKTDYFNE 63
Db 53 TSSGLAAAGLL-CTAL---TACLWGQLPLPWA-SPAQ-----RP 89
QY 64 TTLVWVWF----GTFDLTSCQAMFNLTGCHLTDRSLYNKSHAVLIHHRDI----- 113
Db 90 VSVLLMEPEGGRGHSGKPPDCSLRFNIGSCRLTLDRAAYGAQAQVLEFHRDLVKGPPD 149
QY 114 ---SWDLTNLPOQA-----RPPFQKIWNKLESPHTPOK 145
Db 150 WPPFNAQERTDALELRVFDDEGAVMLAREALETGTSPQQRVWMNFESFHTPGL 209
QY 146 SGI-EHLFNLTLYRRDSDIQVPGFLTVSTNPFVFPVS-----KEKLCVWVSNW 196
Db 210 RGLAKDLFNWTLSTYRDSDLFVPGFLYPRSH- -AEQPSGLPPLARKGLVAVVSHW 267
QY 197 NPEHARVYKYNELSKSTIEHTYQAF-GEYVNDKNLIPTISTCKFYLSPNSIHKDYITE 255
Db 268 NERQARVRYHQLRRHVSVDVFRAGPGQVPVAVGLLHTVARYKFLAFENSQRVDYTE 327
QY 256 KLX-NAFLAGSVPVVLGSPSRENYENIPADSFTHVEDFNSPSELAKYLKEVDKNNKLYLS 314
Db 328 KLWRNFLAGVPPVLGPDNRANTYRFRPGSFTHVDDFPAASLAAYLLFLDRNVAVYRR 387
QY 315 YFNWRKDTVNLPRFWESHACADCHVKRH-QEYKSVGNLEKWF 357
Db 388 YFHWRSYAVHITSFWDPEPCQTCRAVQTSQDQPKSIHNLADWF 431

RESULT 9
Q9R220 PRELIMINARY; PRT; 362 AA.
AC Q9R220;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ALPHA (1,3) FUCOSYLTRANSFERASE 6A.
GN FUT6A.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 35.2%; Score 694; DB 11; Length 362;
Best Local Similarity 41.6%; Pred. No. 3e-45;
```

```
RX MEDLINE=99214609; PubMed=10187834;
RA Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RA Stanley P.;
RT "The gain-of-function chinese hamster ovary mutant LEC11B expresses
RT one of two chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL; AF090450; AAD24888.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41767 MW; 2256EA145B03DA13 CRC64;

Query Match 35.3%; Score 696; DB 11; Length 362;
Best Local Similarity 41.6%; Pred. No. 2.1e-45;
Matches 149; Conservative 65; Mismatches 124; Indels 20; Gaps 10;

QY 10 RPFLIVCIILGCFMACLLIYIKPTNSWVFSPMESASSVLKMKNFSTKTDYF-NEETILV 68
Db 14 RPCLIGLLQLLFCFFSIRVSHDQGPAPDSST-----GPASTPTTTPVPRPFLILL 68
QY 69 WVPFQGTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWDLTN-LPQQARP 126
Db 69 WTPFHSPLTLYPCSKMLPCTADQMTVNSLYPQADAVIFHHRHREISNPSRLPSQRP 128
QY 127 PFKWTWNLSTHTPQKSGIEHLFNLTLYRRDSDIQVPGFLTVSTNPFV---FEVP 183
Db 129 PGQWVWFSESPSHCSRLSALDGYFNLTMSYRSDSDIFTFYGNLEPWAEPVQTVNMS 188
QY 184 SKELKCVWVNNPEHARVYKYNELSKSTIEHTYQAFGEYVNDKNLIPTISTCKFYL 243
Db 189 AKTDLVAVNSNNPKSARVLYYQKQLSHLDVYVGHGHP-LSRGDMGTLLARYKFLA 247
QY 244 FENSIHKDYITEKLY-NAFLAGSVPVVLGSPSRENYENIPADSFTHVEDFNSPSELAKYL 302
Db 248 FENSLHPDYITEKLNKNALEAWAPVVLGSPSRKRYERFLPDFAFIHVDDFSPADLAQYL 307
QY 303 KEVDKNNKLYSFNWRKDTVNLPRFWESHA---CLACDHVKRHQYKSVGNLEKWF 357
Db 308 QKLDKDSQYRYFRWRETLR---PRL-SSMALAFCAQACQLQWDQRYQTVHVSASF 361

RESULT 10
Q9R219 PRELIMINARY; PRT; 362 AA.
AC Q9R219;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALPHA (1,3) FUCOSYLTRANSFERASE 6B.
GN FUT6B.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RA Stanley P.;
RT "The gain-of-function chinese hamster ovary mutant LEC11B expresses
RT one of two chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL; AF090449; AAD24887.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41743 MW; 480D106C40DE5F30 CRC64;

Query Match 35.2%; Score 694; DB 11; Length 362;
Best Local Similarity 41.6%; Pred. No. 3e-45;
```

Matches 149; Conservative 65; Mismatches 124; Indels 20; Gaps 10;

Qy 10 RPFLVCIILGCFMACLLIYIKPTNSWVFSPMESASSVLKMKNFSTKTDYF--NETTILV 68
 Db 14 RPLCIGLLQLLQALCFEFSVIRSHDQGGPPADSDST-----GPASTPTTPVPRPPLILL 68
 Qy 69 WWPFGTQFDLTSCQAMF-NIQGCHLTITDRSLYNKSHAVLIHHRDLSWDLTN-LPQOARP 126
 Db 69 WWPFGTQFDLTSCQAMF-NIQGCHLTITDRSLYNKSHAVLIHHRDLSWDLTN-LPQOARP 126
 Qy 127 PFQKWIWMNLESPTHTPKQSGIEHLNLTITDRSDIOVPYGLFVSTNPFV---FEVP 183
 Db 129 PGQWVWFLESPTHTPKQSGIEHLNLTITDRSDIOVPYGLFVSTNPFV---FEVP 183
 Qy 184 SKEKLVWVSNWNPHEHARVYKYNELSKSIEHTYQAGFGEYVNDKNIPTISTCKEYLS 243
 Db 189 AKTDLVAVSNWNPHEHARVYKYNELSKSIEHTYQAGFGEYVNDKNIPTISTCKEYLS 243
 Qy 244 FENSIHKDYITEKLY-NAFLAGSPVVLGSPSRENYENIPADSFIVEDFNPSSELAAYL 302
 Db 248 FENSLHDIYTEKLYNAFLAGSPVVLGSPSRENYENIPADSFIVEDFNPSSELAAYL 302
 Qy 303 KEVDKNNKLYSPNWRKFTVNLPRFWSHA---CLACDHVKRHKQYKSVGNLEKWF 357
 Db 308 QKLDKDSQSYQRYFRWRETLR---PRL-SSMALAFQACRQLQMDQRYQTVHVSASF 361

RESULT 11

Q9JIK2 PRELIMINARY; PRT; 401 AA.
 ID Q9JIK2 AC Q9JIK2
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.1) (GALACTOSIDE 3-L-
 FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCI-IV).
 GN FUC4.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RX MEDLINE=20166953; PubMed=10700388;
 RA Patnaik S.K., Zhang A., Shi S., Stanley P.;
 RT "Alpha(1,3)fucosyltransferases expressed by the gain-of-function
 Chinese hamster ovary glycosylation mutants LEC12, LEC29, and LEC30.";
 RL Arch. Biochem. Biophys. 375:322-332(2000).
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 THE EXPRESSION OF LEWIS X AND LEWIS Y.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
 ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
 1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 FORM IN TRANS CISTERNAE OF GOLGI.
 DR EMBL: AF221505; AAF82352.1; -
 DR InterPro: IPR001503; GlycoTransf_10.
 DR Pfam: PF00852; GlycoTransf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1
 FT TRANSMEM 24 42 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 85
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 186
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 401 AA; 45309 MW; 3130298017560D13 CRC64;
 Query Match 35.2%; Score 693; DB 11; Length 401;
 Best Local Similarity 41.6%; Pred. No. 4.1e-45;

Matches 142; Conservative 53; Mismatches 96; Indels 50; Gaps 8;

Qy 66 ILVWVWPF---GOTFDLTSCQAMFNTDRSLYNKSHAVLIHHRDLSWDLTNLP 121
 Db 60 VLLWVWPFGRGGHSPSPDCSLRNFISGCRLLTDRAAYGEAQAFLHHRDLVTLGLSDWP 119
 Qy 122 QQ-----ARPPFOKWIWMNLESPTHTPKSG 147
 Db 120 PPWGAQVRDEALBQRVDDQGAAMLAGALETAGSRPPCORVWVWVNFSPSHSPLRG 179
 Qy 148 I-EHLFNLTITDRSDIOVPYGLFVSTNPFV-----KEKLVWVSNWNP 199
 Db 180 LAKNLFNLTITDRSDIOVPYGLFVSTNPFV-----KEKLVWVSNWNP 199
 Qy 200 HARVYKYNELSKSIEHTYQO-AGEYVNDKNIPTISTCKEYLSFENSHTKDYITEKLY 258
 Db 239 QARVYKYNELSKSIEHTYQO-AGEYVNDKNIPTISTCKEYLSFENSHTKDYITEKLY 258
 Qy 259 -NAFLAGSPVVLGSPSRENYENIPADSFIVEDFNPSSELAAYLKYLSYFN 317
 Db 299 RNFALAGAVPVVLGSPSRENYENIPADSFIVEDFNPSSELAAYLKYLSYFN 317
 Qy 318 WRKDFTNLPRFWSHACLDHVKRHH-QEYKSVGNLEKWF 357
 Db 359 WRRSYAVHITSFWDPEWCRCTCAVQTSGDQPKSQIQLASWF 399

RESULT 12

O35886 PRELIMINARY; PRT; 362 AA.
 ID O35886 AC O35886;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ALPHA(1,3)FUCOSYLTRANSFERASE.
 GN ALPHA(1,3)FUT.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99214609; PubMed=10187834;
 RA Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
 Stanley P.;
 RT "The gain-of-function chinese hamster ovary mutant LEC11B expresses
 one of two chinese hamster FUT6 genes due to the loss of a negative
 regulatory factor.";
 RL J. Biol. Chem. 274:10439-10450(1999).
 DR EMBL: U78737; AAB64355.1; -
 DR InterPro: IPR001503; GlycoTransf_10.
 DR Pfam: PF00852; GlycoTransf_10; 1.
 KW Transferase; Glycosyltransferase.
 SQ SEQUENCE 362 AA; 41810 MW; A67940D57D47004C CRC64;
 Query Match 35.0%; Score 689; DB 11; Length 362;
 Best Local Similarity 41.3%; Pred. No. 7.3e-45;
 Matches 148; Conservative 66; Mismatches 124; Indels 20; Gaps 10;
 Qy 10 RPFLVCIILGCFMACLLIYIKPTNSWVFSPMESASSVLKMKNFSTKTDYF--NETTILV 68
 Db 14 RPLCIGLLQLLQALCFEFSVIRSHDQGGPPADSDST-----GPASTPTTPVPRPPLILL 68
 Qy 69 WWPFGTQFDLTSCQAMF-NIQGCHLTITDRSLYNKSHAVLIHHRDLSWDLTN-LPQOARP 126
 Db 69 WWPFGTQFDLTSCQAMF-NIQGCHLTITDRSLYNKSHAVLIHHRDLSWDLTN-LPQOARP 126
 Qy 127 PFQKWIWMNLESPTHTPKQSGIEHLNLTITDRSDIOVPYGLFVSTNPFV---FEVP 183
 Db 129 PGQWVWFLESPTHTPKQSGIEHLNLTITDRSDIOVPYGLFVSTNPFV---FEVP 183
 Qy 184 SKEKLVWVSNWNPHEHARVYKYNELSKSIEHTYQAGFGEYVNDKNIPTISTCKEYLS 243

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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:40:22 ; Search time 25 Seconds
(without alignments)
2484.207 Million cell updates/sec

Title: US-09-744-748-2

Perfect score: 1970

Sequence: 1 WTSTSGILRPPLIVCIILG.....HVKRHQYKSVGNLEKFWN 359

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1970	100.0	359	4 Q9Y231	Q9Y231 homo sapien
2	1961	99.5	359	11 O88819	O88819 mus musculus
3	1954	99.2	359	11 Q9JIG1	Q9JIG1 cricetus
4	1946	98.8	359	11 Q9JIB3	Q9JIB3 rattus norv
5	906.5	46.0	391	13 Q9W640	Q9W640 brachydanio
6	837	42.5	392	13 Q9W641	Q9W641 gallus gall
7	792	40.2	356	13 Q9S952	Q9S952 rattus norv
8	700.5	35.6	433	11 Q9S988	Q9S988 rattus norv
9	692	35.1	362	11 Q9R220	Q9R220 cricetus
10	690	35.0	382	11 Q9R219	Q9R219 cricetus
11	690	35.0	401	11 Q9JIK2	Q9JIK2 cricetus
12	685.5	34.8	386	11 Q920V9	Q920V9 mus musculus
13	685	34.8	362	11 Q35886	Q35886 cricetus
14	685	34.8	390	11 Q920W0	Q920W0 mus musculus
15	684	34.7	390	11 Q920W1	Q920W1 mus musculus
16	684	34.7	390	11 Q920V7	Q920V7 mus musculus

17	684	34.7	390	11 Q91VB5	Q91VB5 mus musculus
18	684	34.7	390	11 Q91V20	Q91V20 mus musculus
19	683	34.7	390	11 Q920V6	Q920V6 mus spicile
20	680	34.5	390	11 Q920V8	Q920V8 mus musculus
21	669	34.0	360	6 Q9XT34	Q9XT34 sus scrofa
22	667	33.9	361	4 Q9PLW6	Q9PLW6 homo sapien
23	664.5	33.7	359	4 Q9UND8	Q9UND8 homo sapien
24	661.5	33.6	359	6 Q9GKU6	Q9GKU6 pongo pygma
25	653	33.1	365	6 Q9TQ03	Q9TQ03 bos taurus
26	579	29.4	351	5 Q76204	Q76204 schistosoma
27	383	19.4	426	5 Q9NJ24	Q9NJ24 schistosoma
28	318	16.1	400	5 Q01906	Q01906 caenorhabdi
29	308	15.6	1652	5 Q22202	Q22202 caenorhabdi
30	299	15.2	312	5 Q9NSH5	Q9NSH5 caenorhabdi
31	281.5	14.3	451	5 Q21362	Q21362 caenorhabdi
32	255	12.9	489	11 Q9CKS9	Q9CKS9 mus musculus
33	231.5	11.8	405	10 Q93X61	Q93X61 beta vulgar
34	219	11.1	268	10 Q93WR9	Q93WR9 medicago tr
35	200	10.2	219	10 Q93WS0	Q93WS0 medicago tr
36	196	9.9	510	10 Q9ST51	Q9ST51 phaseolus a
37	189.5	9.6	445	5 Q9W0F6	Q9W0F6 drosophila
38	170.5	8.7	292	5 Q76544	Q76544 dictyosteli
39	160.5	8.1	183	16 Q92GR3	Q92GR3 rickettsia
40	153.5	7.8	338	2 Q87135	Q87135 vibrio chol
41	153	7.8	475	2 Q9L8S4	Q9L8S4 helicobacte
42	151.5	7.7	346	2 Q87156	Q87156 vibrio chol
43	150.5	7.6	338	2 Q34231	Q34231 vibrio chol
44	142	7.2	478	2 Q30511	Q30511 helicobacte
45	137.5	7.0	333	2 Q32631	Q32631 helicobacte

ALIGNMENTS

RESULT 1

Q9Y231	ID	Q9Y231	PRELIMINARY;	PRT;	359 AA.
AC	Q9Y231;				
DT	01-NOV-1999 (TReMBLrel. 12, Created)				
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)				
DT	01-JUN-2001 (TReMBLrel. 17, Last annotation update)				
DE	ALPHA-3-FUCOSYLTRANSFERASE.				
GN	FUT9.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=WHOLE EMBRYO;				
RA	Caillieu A., Coullin P., Candellier J.J., Balanzino L., Oriol R.,				
RA	Mollicone R.;				
RT	"Cloning, expression and chromosome localization of a human embryonic				
RT	FUT9 transcript."				
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99332063; PubMed=10405152;				
RA	Kaneko M., Kudo T., Iwasaki H., Ikehara Y., Nishihara S., Nakagawa S.,				
RA	Sasaki K., Shina T., Inoko H., Saitou N., Narimatsu H.;				
RT	"Human hepatitis B virus mutants: significance of molecular changes.";				
RL	FEBS Lett. 453:237-242(1999).				
DR	EMBL; AJ238701; CAB41890.1; -				
DR	EMBL; AB023021; BAA81685.1; -				
DR	InterPro: IPR001503; Glyco-transf_10.				
DR	Pfam: PF00852; Glyco-transf_10; 1.				
KW	Transferase; Glycosyltransferase.				
SQ	SEQUENCE 359 AA; 42041 MW; C90CF5C02CB644D9 CRC64;				

June 99.

Query Match 100.0%; Score 1970; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.8e-145;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTSGILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 DB 1 MTSTSGILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 QY 61 FNETTILVWVPFGQTDLTSCQAMFIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 DB 61 FNETTILVWVPFGQTDLTSCQAMFIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 QY 121 PQAARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 DB 121 PQAARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 QY 181 EYPSKEKLVWVSNWNPENHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 DB 181 EYPSKEKLVWVSNWNPENHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 QY 241 YLSFENSIIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 DB 241 YLSFENSIIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPFWESHACLDHVHRHQRHKEYKSVGNLEKFWFN 359
 DB 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPFWESHACLDHVHRHQRHKEYKSVGNLEKFWFN 359

RESULT 2
 O88819 ID O88819 PRELIMINARY; PRT: 359 AA.
 AC O88819;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ALPHA-(1.3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
 DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX) (MFUC-TIX).
 GN FUT9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.. FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=BALE/C; TISSUE=BRAIN;
 RX MEDLINE=98434588; PubMed=9756916;
 RA Kudo T., Ikehara Y., Togayachi A., Kaneko M., Hiraga T., Sasaki K.,
 RA Narimatsu H.;
 RT "Expression cloning and characterization of a novel murine alphanal, 3-
 RT fucosyltransferase, mFuc-TIX, that synthesizes the Lewis x (CD15)
 RT epitope in brain and kidney.";
 RL J. Biol. Chem. 273:26729-26738(1998).
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 CC THE EXPRESSION OF LEWIS X AND LEWIS Y.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
 CC ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
 CC 1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN AND KIDNEY. IT
 CC ALSO EXPRESSED IN THE STOMACH, COLON, UTERUS AND EPIDIDYMIS. NOT
 CC FOUND IN THYMUS, LIVER, SPLEEN, OVARY, LUNG, HEART, TESTIS AND
 CC SMALL INTESTINE.
 DR EMBL; AB015426; BAA33522.1; -.
 DR MGB; MG1:1330859; Fuf9.
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 11
 FT TRANSMEM 12 30
 FT SIGNAL-ANCHOR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 31 359
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 62 62
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 359 AA; 42041 MW; 96A2394547F2A44E CRC64;
 Query Match 99.5%; Score 1961; DB 11; Length 359;
 Best Local Similarity 99.2%; Pred. No. 3.4e-144;
 Matches 356; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTSTSGILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 DB 1 MTSTSGILRPLFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKNFSTKTDY 60
 QY 61 FNETTILVWVPFGQTDLTSCQAMFIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 DB 61 FNETTILVWVPFGQTDLTSCQAMFIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 QY 121 PQAARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 DB 121 PQAARPPQKWIWMNLESPTTPQKSGIEHLNLTLYRRSDIOVPYGLTSTNPFVF 180
 QY 181 EYPSKEKLVWVSNWNPENHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 DB 181 EYPSKEKLVWVSNWNPENHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
 QY 241 YLSFENSIIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 DB 241 YLSFENSIIHKDYITEKLYNAFLAGSVVVLGSPRENYENIPADSFHVEDYNSPELAK 300
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPFWESHACLDHVHRHQRHKEYKSVGNLEKFWFN 359
 DB 301 YLKEVDKNNKLYLSYFNWRKDFTVNLPFWESHACLDHVHRHQRHKEYKSVGNLEKFWFN 359

RESULT 3
 O88819 ID O88819 PRELIMINARY; PRT: 359 AA.
 AC O88819;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ALPHA-(1.3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-
 DE FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 9) (FUCT-IX).
 GN FUT9.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RX MEDLINE=20166953; PubMed=10700388;
 RA Patnaik S.K., Zhang A., Shi S., Stanley P.;
 RA "Alpha(1.3)fucosyltransferases expressed by the gain-of-function
 RT Chinese hamster ovary glycosylation mutants LEC12, LEC29, and LEC30.";
 RL Arch. Biochem. Biophys. 375:322-332(2000).
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 CC THE EXPRESSION OF LEWIS X AND LEWIS Y.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-
 CC ACETYL-D-GLUCOSAMINYL-R = GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-
 CC 1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 DR EMBL; AF230460; AAF82412.1; -.
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 11
 FT TRANSMEM 12 30
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 62 62
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 359 AA; 42071 MW; 9D5CD8BFF07EA902 CRC64;

Query Match 99.2%; Score 1954; DB 11; Length 359;
Best Local Similarity 98.6%; Pred. No. 1.2e-143;
Matches 354; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
DB 1 MTSTSGILRPFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
QY 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
DB 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
QY 121 PQOARPPFKWIWNLESPTHTPKSGIEHLEFNLTLYRRSDIQVPGFGLTVSTNPFV 180
DB 121 PQOARPPFKWIWNLESPTHTPKSGIEHLEFNLTLYRRSDIQVPGFGLTVSTNPFV 180
QY 181 EVPSKEKLVQWVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
DB 181 EVPSKEKLVQWVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
QY 241 YLSPFENSIHKDYITEKLYNAGVLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSELAK 300
DB 241 YLSPFENSIHKDYITEKLYNAGVLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSELAK 300
QY 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWESHACLDHVHQRHKEYKSYGNLEKWFVN 359
DB 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWESHACLDHVHQRHKEYKSYGNLEKWFVN 359

RESULT 4
Q99JB3 PRELIMINARY; PRT; 359 AA.
ID AC Q99JB3
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE ALPHA(1,3)-FUCOSYLTRANSFERASE IX.
GN FUT9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimoda Y., Tajima Y., Osanai T., Katsume A., Kohara M., Kudo T.,
RA Narinatsu H., Osumi N., Sanai Y.;
RT "Expression of Lewis x epitope in embryonic forebrain by regulating
RT alpha1,3-fucosyltransferase IX expression."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=20472964; PubMed=11020213;
RA Baboval T., Henion T., Kinnally E., Smith F.I.;
RT "Molecular cloning of rat alpha1,3-fucosyltransferase IX (Fuc-TIX) and
RT comparison of the expression of fuc-TIV and fuc-TIX genes during rat
RT postnatal cerebellum development."
RL J. Neurosci. Res. 62:206-215(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Smith F.I., Baboval T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049819; BAB40953.1; -
DR EMBL; AF345993; AAK16591.1; -
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 359 AA; 42037 MW; 36984A7BD0C6CC80 CRC64;
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Query Match 98.8%; Score 1946; DB 11; Length 359;
Best Local Similarity 98.3%; Pred. No. 4.9e-143;
Matches 353; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTSTSGILRPFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
DB 1 MTSTSGILRPFLVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLMKKNFFSTKTDY 60
QY 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
DB 61 FNETTILVWVWPGQTFDLTSCQAMFNIQCHLTTRDSLYNKSHAVLIHHRDISWDLTNL 120
QY 121 PQOARPPFKWIWNLESPTHTPKSGIEHLEFNLTLYRRSDIQVPGFGLTVSTNPFV 180
DB 121 PQOARPPFKWIWNLESPTHTPKSGIEHLEFNLTLYRRSDIQVPGFGLTVSTNPFV 180
QY 181 EVPSKEKLVQWVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
DB 181 EVPSKEKLVQWVSNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNIPTISACKF 240
QY 241 YLSPFENSIHKDYITEKLYNAGVLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSELAK 300
DB 241 YLSPFENSIHKDYITEKLYNAGVLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSELAK 300
QY 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWESHACLDHVHQRHKEYKSYGNLEKWFVN 359
DB 301 YLKEVDKNNKLYLSYFNWRKDFVNLPRFWESHACLDHVHQRHKEYKSYGNLEKWFVN 359

RESULT 5
Q9W640 PRELIMINARY; PRT; 391 AA.
ID AC Q9W640
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE ALPHA(1,3)-FUCOSYLTRANSFERASE.
GN FT1 OR ZFT1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kageyama N., Natsuka S., Hase S.;
RT "Molecular cloning and characterization of two zebrafish
RT alpha(1,3)-fucosyltransferase genes developmentally regulated in
RT embryogenesis."
RL J. Biochem. 0:0-0(1999).
DR EMBL; AB023627; BAA76706.1; -
DR ZFIN; ZDB-GENE-990715-17; ft1.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 391 AA; 45265 MW; 98826D0B3D9679C2 CRC64;

Query Match 46.0%; Score 906.5; DB 13; Length 391;
Best Local Similarity 45.3%; Pred. No. 2e-62;
Matches 177; Conservative 59; Mismatches 116; Indels 39; Gaps 6;

QY 1 MTSTSGILRPFLVCIILGCFMACLLIYIKPTNSWIFSP-----MESASSVLMK 50
DB 6 LTPPSKA-AQKVIATFELISFVCIFFVYVNPNTFFKFPADVHTNCSTCTCLDVLK 64
QY 51 KNFST-----KDYFNETILVWVWPGQTFDLTSCQAMFNI 88
DB 65 QNYKCTIKNASDNPSTTPAPNPAPATAKDD--QETILLIWWYFPGAREDLGCGSOFNI 122
QY 89 QGCHLTTRDSLYNKSHAVLIHHRDISWDLTNLQOARPPFKWIWNLESPTHTPKSGI 148
DB 123 HGCHLTTRDSLYNKSHAVLIHHRDISWDLTNLQOARPPFKWIWNLESPTHTPKSGI 179
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Matches	148;	Conservative	66;	Mismatches	124;	Indels	20;	Gaps	10;
QY	10	RPFLIVCIIGCFMACLLIYIKPTNSWIFSPMESASSVLKMKNFSTKTYDF-NETILV	68						
Db	14	RPCLIGLIGLQALLFALCFPSYIRVSHDQGGPPADSS- ----GFASTPTTVPVPEFILL	68						
QY	69	VWDFPGQTFDITSCOAMP-NIQCHLTDRSLYNKSHAVLIHHRDISWDLTN-LPQARP	126						
Db	69	WTWDFHSPFLIPLFCCKMLPGTADCOMTVNRSLPQADAVTFHHRDISPNRSLPSQPR	128						
QY	127	PFQKIWIWNLESPTHTPOKSGIEHFNLTITYRDSIDIQVYGLFVSTNPFV- --FEVP	183						
Db	129	PGQRWVFSLESPTSHCSRLSALDGHFNLTMSYSDSDIFTPYGLWLEPVPVQTVNMS	188						
QY	184	SKERLCVCWVYNNNPEHARVYKNELSKSTIITYGOAFGEYVNDKNLPTISACFYLS	243						
Db	189	AKTDLVAVAYNNNPKRSARVLYYKQLSHLVNDVYGHMP-USRGGMGTILARYFYLA	247						
QY	244	FENSIHKDYITEKLY-NAFLAGSVPVVVLGSPSRNENYIPASFIIVEYDNGSPSELA	302						
Db	248	FENSLHPDXTITEKLWKNALAEAWPVVLGSRKNYERFLPPDAFIIVDDFSPADLAQ	307						
QY	303	KEYDKNNKLYLSYFNWKDFTVNLPRFWSHA- --CLADHYKRRHQEYKSVGNLEKWF	357						
Db	308	QKLDKDSQSYORYFRWRKTLR- --PRL-SSMALAFQACROLOWDORYTIVHSVASWF	361						
RESULT 11									
QY	Q9JIK2	PRELIMINARY; PRT: 401 AA.							
AC	Q9JIK2								
DT	01-OCT-2000	(TREMBLrel. 15, Created)							
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)							
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)							
DT	01-JUN-2001	(FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV).							
GN	EN	Fih.							
OS	CC	Cellulatus griseus (Chinese hamster).							
OC	CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	CC	Mammalia; Theria; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;							
OC	CC	Cricetulus							
OX	CC	NCBI_taxid=10029;							
OX	CC	[1]							
RP	CC	SEQUENCE FROM N.A.							
RP	CC	TISSUE=OVARY;							
RR	CC	MEDLINE=20166953; PubMed=10700388;							
RR	CC	Patnak S.K. Zhang A., Shi S., Stanley P.;							
RR	CC	"Alpha(1,3)fucosyltransferases expressed by the gain-of-function							
RR	CC	Chinese hamster ovary 1 fucosylation mutants LEC12, LEC29, and LEC30."							
RR	CC	Arch. Biochem. Biophys. 375:322-332(2000).							
CC	CC	-1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN							
CC	CC	THE EXPRESSION OF LEWIS AND LEWIS X.							
CC	CC	-1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,4-BETA-D-GALACTOSYL-N-							
CC	CC	ACETYL-D-GLUCOSAMINYL-R -> GDP + 1,4-BETA-D-GALACTOSYL-(ALPHA-							
CC	CC	1,3-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.							
CC	CC	-1- SUBCELLULAR LOCATION.							
CC	CC	FORM IN TRANS CISTERNAE OF GOLGI.							

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QY 261 FLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSSELAKEYLKEVDKNNKLYLSYENWRK 320
DB 294 FLAGAVPVVLGPDPRANERVPFGAFTHVDFFNAASLAAYLLFLDRNAVAVRYFRWR 353
QY 321 DFTVNLPRFWESHACLDCHVK 342
DB 354 SFAVHITSFWDEQWCRTCQAVQ 375

RESULT 13
O35886 PRELIMINARY; PRT; 362 AA.
AC O35886;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DE ALPHA(1.3)FUCOSYLTRANSFERASE.
GN ALPHA(1.3)FUT.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99214609; PubMed=10187834;
RA Zhang A., Potvin B., Zaiman A., Chen W., Kumar R., Phillips L.,
RA Stanley P.;
RT "The gain-of-function chinese hamster ovary mutant LEC1B expresses
RT one of two chinese hamster FUT6 genes due to the loss of a negative
RT regulatory factor.";
RL J. Biol. Chem. 274:10439-10450(1999).
DR EMBL; U78737; AAB64355.1; -.
DR InterPro; IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferrase; Glycosyltransferase.
SQ SEQUENCE 362 AA; 41810 MW; A67940D57D47004C CRC64;

Query Match 34.8%; Score 685; DB 11; Length 362;
Best Local Similarity 41.1%; Pred. No. 2.7e-45;
Matches 147; Conservative 67; Mismatches 124; Indels 20; Gaps 10;

QY 10 RPFLVICILGCMACLLIYIKPTNSWIFSPMESASSVLKMKNFSTKDYF-NEITVLY 68
DB 14 RPLGLILLQLLFCALCFSTIRVSHDQGGPADDSPT----GPASPTTPVPRPFIILL 68
QY 69 WVPFGQTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWDLTN-LPQQARP. 126
DB 69 WTAFHRPLTLYPCSKMLPCTADCQMTVNSLYPQADAVIFHREISPNRSLLPQRP 128
QY 127 PFQKIWMNLESTHTPKSGIEHLNLTLYRRSDIQVPGFLTVSTNPFV---FEVP 183
DB 129 PGQRWVWFSLESFSSRLSALDGYNLNLSYRSDDSIPTFYGWLEPWAEPVQTVNMS 188
QY 184 SKEKLVCWVYNNPHEARVKKYNELSKSTEIHTYQAGFYNDKNIPTISACKFYL 243
DB 189 AKTDLVANAVSNPNKSAARVLYIKQLSHLVVDVYGRHMP-USRGMGTLLARYKFLA 247
QY 244 FENSIHKDYITEKLY-NAFLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSSELA 302
DB 248 FENSLHPDYITEKLWNKALEAWPVVLGSPSRKNYERFLPDAFIHVDDEFSPADLAQYL 307
QY 303 KEVDKNNKLYLSTFNWRKDTVNLPRFWESHA---CLACDHVRKHQYKSVGNLEKWF 357
DB 308 QKLDKDSQSYQRYFRWRETLR---PRL-SSMALAFQACQRLQWDQRIQTVHVSASF 361

RESULT 14
Q920W0 PRELIMINARY; PRT; 390 AA.
AC Q920W0;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

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DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
GN ALPHA 1.3-FUCOSYLTRANSFERASE (FRAGMENT).
DE FUT4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6M/2MSF;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039125; BAB68649.1; -.
KW Transferrase; Glycosyltransferase.
FT NON_TER 1
FT NON_TER 390
SQ SEQUENCE 390 AA; 44435 MW; EE7FAE238A5F9530 CRC64;

Query Match 34.8%; Score 685; DB 11; Length 390;
Best Local Similarity 42.1%; Pred. No. 2.9e-45;
Matches 142; Conservative 49; Mismatches 94; Indels 52; Gaps 8;

QY 66 ILVWVMPF---GOTFDLTSCQAMFNIQGCCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
DB 56 VLLWPEFRGRGGYKPSPPDCSLRFNISGCRLLTDRAAYGEAQAVLFHHRDLVKELDWP 115
QY 122 QQ-----ARPPFQKWIWMNLESPTHTPKSG 147
DB 116 PWCARERTKALVLRVFDDEQAVTLTGKALETVGSRPQQRWVWVNFSPSTHTPLRG 175
QY 148 I-EHLFNLTLTYRRSDIQVPGFLTVSTNPFVFEVPS-----KEKLVCVWVYNNP 198
DB 176 LAKDLFNWLTLSYRSDSVFVPGFLYSRSDP--TEQPSGLGPQLARKRGLVAVVYNNWE 233
QY 199 EHARVKKYNELSKSTEIHTYQCAF-GEYVNDKNIPTISACKFYLSTFENSHTKDYITEKL 257
DB 234 HQARVYHQLSRHVSVDVFGTGPGRVPAIGLLHVVARYKFYAFENSRHVDYITEKL 293
QY 258 Y-NAFLAGSPVVLGSPSRENYENIPADSFTHVEDYNSPSSELAKEYLKEVDKNNKLYSYF 316
DB 294 WRNFALAGVPLGPDPRANERVPFGAFTHVDFFNAASLAAYLLFLDRNVSVYRYF 353
QY 317 NWKRDFTVNLPRFWESHACLDCHVKRH-QEYKSVGN 352
DB 354 RWRSEFAVHITSFWDEQWCRTCQAVQTSQDQPKSIHN 390

RESULT 15
Q920W1 PRELIMINARY; PRT; 390 AA.
AC Q920W1;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE ALPHA 1.3-FUCOSYLTRANSFERASE (FRAGMENT).
GN FUT4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10SNJ;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039124; BAB68648.1; -.
KW Transferrase; Glycosyltransferase.
FT NON_TER 1
FT NON_TER 390
SQ SEQUENCE 390 AA; 44435 MW; EE7FAE238A5F9530 CRC64;

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	691.5	35.1	405	1	US-07-914-281-8	Sequence 8, Appli
2	691.5	35.1	405	1	US-08-393-246-8	Sequence 8, Appli
3	691.5	35.1	405	1	US-08-525-058A-8	Sequence 8, Appli
4	691.5	35.1	405	2	US-08-696-731-8	Sequence 8, Appli
5	691.5	35.1	405	4	US-09-042-531-8	Sequence 8, Appli
6	677.5	34.4	405	2	US-08-483-151-4	Sequence 4, Appli
7	670	34.0	299	5	PCR-US91-00899-6	Sequence 6, Appli
8	670	34.0	361	1	US-07-914-281-2	Sequence 2, Appli
9	670	34.0	361	1	US-08-393-246-2	Sequence 2, Appli
10	670	34.0	361	1	US-08-273-411-3	Sequence 3, Appli
11	670	34.0	361	1	US-08-525-058A-2	Sequence 2, Appli
12	670	34.0	361	2	US-08-696-731-2	Sequence 2, Appli
13	670	34.0	361	4	US-09-042-531-2	Sequence 2, Appli
14	670	34.0	361	5	PCR-US91-00899-7	Sequence 7, Appli
15	670	34.0	374	1	US-07-914-281-11	Sequence 11, Appli
16	670	34.0	374	1	US-08-393-246-11	Sequence 11, Appli
17	670	34.0	374	1	US-08-525-058A-11	Sequence 11, Appli
18	670	34.0	374	2	US-08-696-731-11	Sequence 11, Appli
19	670	34.0	374	4	US-09-042-531-11	Sequence 11, Appli
20	665.5	33.8	359	1	US-07-914-281-14	Sequence 14, Appli
21	665.5	33.8	359	1	US-08-393-246-14	Sequence 14, Appli
22	665.5	33.8	359	1	US-08-525-058A-14	Sequence 14, Appli
23	665.5	33.8	359	2	US-08-696-731-14	Sequence 14, Appli
24	665.5	33.8	359	4	US-09-042-531-14	Sequence 14, Appli
25	651.5	33.1	357	5	PCR-US91-00899-14	Sequence 14, Appli
26	582	29.5	342	2	US-08-483-151-2	Sequence 2, Appli
27	103.5	5.3	1088	2	US-08-742-026-2	Sequence 2, Appli

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Db 28 VCVLAAGLCTALITYACWQQLPPLWA-SPTDS-----RPGVLL 68
Qy 69 WVPFGQTFDL-----TSCQAMNIQGGCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115
Db 69 WVEPFGGRSDAPRPPDCPLRFNISGCRLLTDRASYGEAQAVLFHHRDLVKGPDPWPPW 128
Qy 116 -----DLTNLPQO-----ARPPFKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDLRLVDEEAAAAEALATSPRPPGQRWVMNFESPSHSGPLSLASNL 188
Qy 152 FNLTLYRDSIOVPYGFVLTSTNPFVFEVPS-----KEKLVCMVVSNNWPEHARV 203
Db 189 FNWTLSYRADSDVPYGYLYPRSH--GDPPSGLAPLSRKQGLVAVVWSHWDQARV 246
Qy 204 KYNELSKSIEIHTYQAF-GEYVNDKNLPTISTCKFYLSFENS IHKDYITEKLY-NAF 261
Db 247 RYHQLSHQVTVDFGRGQGPVPEIGLLHTVARYKFLAFENSQHLDTYTEKLWRLAL 306
Qy 262 LAGSVVVLGSPRENYENIPADSFIVHEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDNRYERFVPRGAFIHVDPPSASSLASLYLLFLDRNPAYVRYRHFHRRS 366
Qy 322 FTVNLPFWESHACLADHKVRHGOEY-KSVGNLEKWF 357
Db 367 YAVHITSEWDEPWCRCVQAVQAGDRPKSIRNLASWF 403

RESULT 2
US-08-393-246-8
; Sequence 8, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS.
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C. Jefferson Davis Highway, Fourth Floor
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
US-08-393-246-8
Query Match 35.1%; Score 691.5; DB 1; Length 405;
Best Local Similarity 38.8%; Pred. No. 2.1e-58;
Matches 154; Conservative 58; Mismatches 110; Indels 75; Gaps 14;

Qy 15 VCIILGCFMAC--LLIYI---KPTNSWVFSPMESASSVLKMKNFSTKTDYFNETTILV 68
Db 28 VCVLAAGLCTALITYACWQQLPPLWA-SPTDS-----RPGVLL 68
Qy 69 WVPFGQTFDL-----TSCQAMNIQGGCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115
Db 69 WVEPFGGRSDAPRPPDCPLRFNISGCRLLTDRASYGEAQAVLFHHRDLVKGPDPWPPW 128
Qy 116 -----DLTNLPQO-----ARPPFKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDLRLVDEEAAAAEALATSPRPPGQRWVMNFESPSHSGPLSLASNL 188
Qy 152 FNLTLYRDSIOVPYGFVLTSTNPFVFEVPS-----KEKLVCMVVSNNWPEHARV 203
Db 189 FNWTLSYRADSDVPYGYLYPRSH--GDPPSGLAPLSRKQGLVAVVWSHWDQARV 246
Qy 204 KYNELSKSIEIHTYQAF-GEYVNDKNLPTISTCKFYLSFENS IHKDYITEKLY-NAF 261
Db 247 RYHQLSHQVTVDFGRGQGPVPEIGLLHTVARYKFLAFENSQHLDTYTEKLWRLAL 306
Qy 262 LAGSVVVLGSPRENYENIPADSFIVHEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDNRYERFVPRGAFIHVDPPSASSLASLYLLFLDRNPAYVRYRHFHRRS 366
Qy 322 FTVNLPFWESHACLADHKVRHGOEY-KSVGNLEKWF 357
Db 367 YAVHITSEWDEPWCRCVQAVQAGDRPKSIRNLASWF 403

RESULT 3
US-08-525-058A-8
; Sequence 8, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,058A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
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FILING DATE: 20-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Lavalleye, Jean-Paul M. P.
 REGISTRATION NUMBER: 31,451
 REFERENCE/DOCKET NUMBER: 2363-060-55
 TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-4500
TELEFAX: (703) 486-2347
TELEX: 248855 OPAT UR

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-696-731-8

Query Match 35.1%; Score 691.5; DB 2; Length 405;
Best Local Similarity 38.8%; Pred. No. 2.1e-58;
Matches 154; Conservative 58; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI----KPTNSWVSPMESASSVLKMKMNFSTKTDYFNETHILV 68
   ||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 28 VCVLAAAGLTCTALITACWGQLPPLPWA-SPTPS-----RPVGVLL 68

QY 69 WVPFGGTFDL----TSCQMFNIQGCCHLITDRSLYKNSHAVLIHHRDI-----SW---- 115
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 69 WVEPFGGRDSAPRPDPDCLPRFNISGCRLLTDASYGQAQVLFHHRDLVKGPDPWDPWP 128

QY 116 -----DLNLPOQ-----ARPPFKWIMNLESPTHP-QKSGTEHL 151
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 129 GIQHTAEFVDLRLVDEEAAAAAALATSSPRPGQRVWMNFESHSFGLSLASNL 188

QY 152 FNLTLYRRDSDIQVPYGFLLTSTNPFVFPVS-----KEKLVCWVSNWNPEHARV 203
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 189 FNWTLTSYRADSDVEVPYGYLPRSHP--GPPPSGLAPPLSRKQGLVAWVYSHWDERQARV 246

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Db 247 RYTHQLSQHTVVDVFGRRGGQCPVPEIGLHTVARYKFYLAFENSQHLDYITEKLWRNAL 306
QY 262 LAGSVPVVLGSPSRENENYIPADSFIVHEDFNSPELAKYLYKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAPVVLGPDRAHYERFVRGAFIHVDDEPSASSLASLYLLFLDRNPAYRRYFHWRRS 366
QY 322 FTWNLPRFWSHACLADCHVKRHOEY - KSVGNLEKWF 357
Db 367 YAVHITSFWEDEPCWRCVQAVQAGDRPKSIRNLASWF 403

RESULT 5
US-09-042-531-8
; Sequence 8, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLAT
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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US-09-042-531-8
; Sequence 8, Application US/09042531

Patent No. 6268193

GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B.

;
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS.

10 TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLAT

; ;
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRU
; NUMBER OF SEQUENCES: 14

;
; CORRESPONDENCE ADDRESS :
; ADDRESSEE: ORION SPITVAK MCCLELLAND WATER & NUTRITION

ADDRESSEE: OGDON, STEVEN, MCCLELLAND, MARK & NEOSIADI,
; ADDRESSEE: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042.531
FILING DATE: 30-MAR-1994
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US/08/393,246
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lavallee, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-042-531-8

Query Match 35.1%; Score 691.5; DB 4; Length 405;
Best Local Similarity 38.8%; Pred. No. 2.1e-58;
Matches 154; Conservative 58; Mismatches 110; Indels 75; Gaps 14;
QY 15 VCIIILGCFMAC--LLIYI---KFTNSWVSPMESASSVLKMKNFSTKTDYFNETTILV 68
DB 28 VCVLAAGSLTCTALITYACWGQLPPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQFDL-----TSCQAMENIOGCHLTDRSLYKNSHAVLIHHRDI-----SW--- 115
DB 69 WWPFGGDSAPRPDPDCPLRFNLSGCLLTDASYGEAQVLFHHRDLVKGPPDPWPPW 128
QY 116 -----DLTNLPQ-----ARPPFKWIMNLESTHTP-QKSGIEHL 151
DB 129 GIOHTAEVDLRLVDYEEAAAAEALATSSPRPRKRWMMNFESPSHSGLSASNL 188
QY 152 FNLTLYRRSDIOVPYGFVLTSTNPFVFEVPS-----KEKLVGVVSNWNPHEARV 203
DB 189 FNWTLISYRADSDVFPYGYLPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEHTYQAF-GEYVNDKNLPTISTCKFYLSFENSIRKDYITEKLY-NAF 261
DB 247 RYHQLSQHVTVDVFGGPGQPVEIGLLHTVARYKYLAFENSQHLDYITEKLWRNL 306
QY 262 LAGSPVVLGSPRENYENIPADSFHVEDFNSPSELAKYLKVEDKNKLYLSYFNWRKD 321
DB 307 LAGAVPVVLGPDRAHYERFVRGAFIHVDOPFSASSLSAYLLFLDRNPVAVRYRHHWRS 366
QY 322 FTVNLPWFESHACLDHVKRHOEY-KSVGNLEKWF 357
DB 367 YAVHITSFWEPCWRCVQAVQAGDRPKSIRNLASWF 403

RESULT 6
US-08-483-151-4
Sequence 4, Application US/08483151
Patent No. 5858752
GENERAL INFORMATION:
APPLICANT: Seed, Brian
TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.151
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F. 35,238
REGISTRATION NUMBER: 00786/278001
REFERENCE/DOCKET NUMBER: 00786/278001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-151-4
Query Match 34.4%; Score 677.5; DB 2; Length 405;
Best Local Similarity 38.0%; Pred. No. 4.7e-57;
Matches 151; Conservative 60; Mismatches 111; Indels 75; Gaps 14;
QY 15 VCIIILGCFMAC--LLIYI---KFTNSWVSPMESASSVLKMKNFSTKTDYFNETTILV 68
DB 28 VCVLAAGSLTCTALITYACWGQLPPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQFDL-----TSCQAMENIOGCHLTDRSLYKNSHAVLIHHRDI-----SW--- 115
DB 69 WWPFGGSAISAPRPDPDCPLRFNLSGCLLTDASYGEAQVLFHHRDLVKGPPDPWPPW 128
QY 116 -----DLTNLPQ-----ARPPFKWIMNLESTHTP-QKSGIEHL 151
DB 129 GIOHTAEVDLRLVDYEEAAAAEALATSSPRPRKRWMMNFESPSHSGLSASNL 188
QY 152 FNLTLYRRSDIOVPYGFVLTSTNPFVFEVPS-----KEKLVGVVSNWNPHEARV 203
DB 189 FNWTLISYRADSDVFPYGYLPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEHTYQAF-GEYVNDKNLPTISTCKFYLSFENSIRKDYITEKLY-NAF 261
DB 247 RYHQLSQHVTVDVFGGPGQPVEIGLLHTVARYKYLAFENSQHLDYITEKLWRNL 306
QY 262 LAGSPVVLGSPRENYENIPADSFHVEDFNSPSELAKYLKVEDKNKLYLSYFNWRKD 321
DB 307 LAGAVPVVLGPDRAHYERFVRGAFIHVDOPFSASSLSAYLLFLDRNPVAVRYRHHWRS 366
QY 322 FTVNLPWFESHACLDHVKRHOEY-KSVGNLEKWF 357
DB 367 YAVHITSFWEPCWRCVQAVQAGDRPKSIRNLASWF 403
RESULT 7
PCT-US91-00899-6
Sequence 6, Application PC/TUS9100899
GENERAL INFORMATION:
APPLICANT: Lowe, John B.
TITLE OF INVENTION: Method and Products For the Synthesis of
TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
TITLE OF INVENTION: Genetic Sequences That Determine These Structures
NUMBER OF SEQUENCES: 16

;; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
;; TITLE OF INVENTION: GLYCOPOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
;; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESS: P.C.
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/393,246
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/220,433
;; FILING DATE: 30-MAR-1994
;; APPLICATION NUMBER: US 07/914,281
;; FILING DATE: 20-JUL-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-4500
;; TELEX: (703)486-2347
;; FAX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 361 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-393-246-2

Query Match 34.0%; Score 670; DB 1; Length 361;
Best Local Similarity 43.4%; Pred. No. 2.le-56;
Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;

Qy 66 ILVWVWPFQGTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
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Qy 120 LPQOARPPFKWIMWNLESPTHTPQKSGIEHLNLTLYRRSDSIQVPGFLTV-STNPF 178
Db 121 LPPSPRQOGQWIFNLEPPPCQHLALDRYFNLMTSYRSDSDIFTYPGWLEPWSGQPA 180
Qy 179 --VFEVPSKEKLVCMVYNNWNPENHARVYKYNELSKSIEHTYGOAFGEYVNDKNLIPTIS 236
Db 181 HPPLNLSAKTELVAWAVSNWPKDSARVRYQSLQAHKVDVYGRSH-KPLPKGTMMETLS 239
Qy 237 TCKYLSFENSIIHKDYITEKLY-NAFLAGSVPVVGLGSRNENYIPADSFHVEDFNSP 295
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Qy 296 SELAKYLEVDNKNKLSYFNWKRDTVNLPR--FWSHACIACDHWKHEQYKSGVNL 353
Db 300 KDLARYLQELDKHARYLSYFNWRETUR---PRFSWALDFCKACWKLQOESRYQTVRSI 356
Qy 354 EKWF 357
Db 357 AAWF 360

RESULT 10

US-08-273-411-3
;; Sequence 3, Application US/08273411
;; Patent No. 5625124
;; GENERAL INFORMATION:
;; APPLICANT: Falk, per
;; APPLICANT: Gordon, Jeffrey I.
;; TITLE OF INVENTION: Animal Model for Gastro-Intestinal
;; TITLE OF INVENTION: Disease
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Patrea L. Pabst
;; STREET: 1100 Peachtree Street, Suite 2800
;; CITY: Atlanta
;; STATE: Georgia
;; COUNTRY: USA
;; ZIP: 30309-4530
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/273,411
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: WU106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 815-6508
;; TELEFAX: (404) 815-6555
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 361 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1..361
;; OTHER INFORMATION: /note= "GDP-L-fucose:beta-D-N-acetylglucosaminide-3,4-alp
;; PUBLICATION INFORMATION:
;; AUTHORS: Kukowska-Latallo, et al.
;; JOURNAL: Genes & Development
;; VOLUME: 4
;; PAGES: 1288-1303
;; DATE: 1990
;; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 361
US-08-273-411-3

Query Match 34.0%; Score 670; DB 1; Length 361;
Best Local Similarity 43.4%; Pred. No. 2.le-56;
Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;

Qy 66 ILVWVWPFQGTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
Db 65 ILLWTWPFHPIVALSRCSEMVPGTADCHITADRKVYQADTVIVHH-----WDIMSNPKSR 120
Qy 120 LPQOARPPFKWIMWNLESPTHTPQKSGIEHLNLTLYRRSDSIQVPGFLTV-STNPF 178
Db 121 LPPSPRQOGQWIFNLEPPPCQHLALDRYFNLMTSYRSDSDIFTYPGWLEPWSGQPA 180
Qy 179 --VFEVPSKEKLVCMVYNNWNPENHARVYKYNELSKSIEHTYGOAFGEYVNDKNLIPTIS 236
Db 181 HPPLNLSAKTELVAWAVSNWPKDSARVRYQSLQAHKVDVYGRSH-KPLPKGTMMETLS 239
Qy 237 TCKYLSFENSIIHKDYITEKLY-NAFLAGSVPVVGLGSRNENYIPADSFHVEDFNSP 295
Db 300 KDLARYLQELDKHARYLSYFNWRETUR---PRFSWALDFCKACWKLQOESRYQTVRSI 356
Qy 354 EKWF 357
Db 357 AAWF 360

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Qy	296	SELAKYLEKVEDKNKNKLYLSYFNWRKDOFTVNLPR--FWESHACIACADHVVRKHQGYKSVGNL	353
Db	300	KDLARYLQELDKDHARYLSYFWRRETLR--PRSFWMALDFCKACWKLQOESRYQYTVRSI	356
Qy	354	EKWF	357
Db	357	AAWF	360

RESULT 11
 US-08-525-058A-2
 ; Sequence 2, Application US/08525058A
 ; Patent No. 5770420
 ; GENERAL INFORMATION:
 ; APPLICANT: LOWE, JOHN B.
 ; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
 ; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
 ; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
 ; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLOM, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 ; STREET: 1755 Jefferson Davis Highway, Fourth Floor
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/525,058A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lavalleye, Jean-Paul M. P.
 ; REGISTRATION NUMBER: 31,451
 ; REFERENCE/DOCKET NUMBER: 2363-060-55
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)521-4500
 ; TELEFAX: (703)486-2347
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-525-058A-2

[illegible][illegible]

QY 179 --VFEPVSKELVWVSNMPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTIS 236
Db 181 HPLNLAKTELAVAWSNMKNPDSARVYQSLQAHKVDVYGRSH-KPLPKGTMMETLS 239
QY 237 TCKFYLSFENSIHKDYITEKLY-NAFLAGSVPVVLGSPRSRENYENYIPADSFIVHEDFNSP 295
Db 240 RYKFLAFENSLHPDYITEKLNRNALEAWAVPVVLGSPRSNYERFLPPDAFIHVDQFSP 299
QY 296 SELAKYLKEVDKNNKLYSYFNWRKDFTVNLPR--FWESHACIACDHRVRRHQYKSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRSFWSALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
Db 357 AAWF 360

RESULT 13
US-09-042-531-2
; Sequence 2, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOPOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,531
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-042-531-2

Query Match 34.0%; Score 670; DB 4; Length 361;
Best Local Similarity 43.4%; Pred. No. 2.1e-56;
Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;

QY 66 ILVWVWPGFTDLTSCQAMF-NIQGCHITTRSLYKSHAVLIHHRDISWDL-----TN 119

Query Match 34.0%; Score 670; DB 5; Length 361;
Best Local Similarity 43.4%; Pred. No. 2.1e-56;

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QY 179 --VFEPVSKELVWVSNMPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTIS 236
Db 181 HPLNLAKTELAVAWSNMKNPDSARVYQSLQAHKVDVYGRSH-KPLPKGTMMETLS 239
QY 237 TCKFYLSFENSIHKDYITEKLY-NAFLAGSVPVVLGSPRSRENYENYIPADSFIVHEDFNSP 295
Db 240 RYKFLAFENSLHPDYITEKLNRNALEAWAVPVVLGSPRSNYERFLPPDAFIHVDQFSP 299
QY 296 SELAKYLKEVDKNNKLYSYFNWRKDFTVNLPR--FWESHACIACDHRVRRHQYKSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRSFWSALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
Db 357 AAWF 360

RESULT 14
PCT-US91-00899-7
; Sequence 7, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: LOWE, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOPOLIPIDS,
; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
; TITLE OF INVENTION: Genetic Sequences That Determine These Structur
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00899
; FILING DATE: 19910214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye Ph.D., Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-5940
; TELEFAX: (703)486-2347
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Blood
; CELL LINE: A431
PCT-US91-00899-7

Query Match 34.0%; Score 670; DB 5; Length 361;
Best Local Similarity 43.4%; Pred. No. 2.1e-56;

	Matches	132:	Conservative	57:	Mismatches	99:	Indels	12:	Gaps	8:	
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Qy	181	EVPSKEKL	VCWVSVNWNPE	HAUKVYYNELSKS	IEIHYGQAFG	YVNDKKNLIP	ISTCKF	240			
Db	198	NLSAKTEL	VAWAVSNWKP	SARVRYQSLQ	AHLKVDVYGRSH	-	KPLPKGTMMETLS	RYKF	256		
Qy	241	YLSFENSI	HKDYITEKLY	-	NAFLAGSVPV	VLGSPRENYENIP	ADSITHVDFD	NPSELA	299		
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Job time : 22 secs

Search completed: October 8, 2002, 18:52:18
Job time : 22 secs

RESULT 15
US-07-914-281-11
; Sequence 11, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/914,281
; FILING DATE: 19920720
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-914-281-11

Query Match	34.0%;	Score 670;	DB 1;	Length 374;
Best Local Similarity	44.0%;	Pred. No. 2.2e-56;		

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:05:27 ; Search time 42.5 Seconds
(without alignments)
938.247 Million cell updates/sec

Title: US-09-744-748-2
Perfect score: 1970
Sequence: 1 WTSTSGILRPLIVCIILG.....HVKRHQEYKSVNLEKFWFN 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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	22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*		

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	100.0	359	21	AA1980996
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3	689.5	35.0	405	11	AA1981119
4	689.5	35.0	405	12	AA1981352
5	689.5	35.0	405	12	AA1981404
6	689.5	35.0	405	13	AA1982840
7	689.5	35.0	530	12	AA1984405
8	685.5	34.8	405	15	AA1984937
9	685.5	34.8	405	18	AA1983641
10	681.5	34.6	405	18	AA1981821
11	676	34.3	360	18	AA19814515

12	675	34.3	360	18	AA19814514	Human chimeric fuc
13	674	34.2	361	18	AA19814530	Human chimeric fuc
14	673	34.2	361	18	AA19814520	Human chimeric fuc
15	672	34.1	361	18	AA19814517	Human chimeric fuc
16	671	34.1	360	18	AA19814516	Human chimeric fuc
17	669.5	34.0	359	18	AA19814523	Human chimeric fuc
18	669	34.0	360	18	AA19814526	Human chimeric fuc
19	668	34.0	496	15	AA19814538	A glycosyltransferase
20	668	33.9	361	18	AA19814519	Human chimeric fuc
21	667	33.9	361	12	AA19813749	GDP-Fuc:[beta-D-Ga
22	667	33.9	361	15	AA19814534	A glycosyltransferase
23	667	33.9	361	18	AA19823806	Human alpha 1,3/4
24	667	33.9	361	18	AA19814527	Human chimeric fuc
25	667	33.9	361	18	AA19813638	Human alpha(1,3)/1,
26	667	33.9	361	22	AA19814542	Human Lewis enzyme
27	667	33.9	374	15	AA19814539	A glycosyltransferase
28	667	33.9	374	18	AA19813642	Human alpha(1,3)-f
29	662.5	33.6	359	15	AA19814533	Alpha-(1-3)Fuc-Tv1
30	662.5	33.6	359	18	AA19814529	Human chimeric fuc
31	662.5	33.6	359	18	AA19813643	Human chimeric fuc
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33	660.5	33.5	360	18	AA19814528	Human chimeric fuc
34	660	33.5	361	18	AA19814518	Human chimeric fuc
35	658.5	33.4	360	18	AA19814521	Human chimeric fuc
36	657.5	33.4	359	18	AA19814522	Human chimeric fuc
37	656.5	33.3	359	18	AA19814525	Human chimeric fuc
38	655.5	33.3	359	18	AA19814531	Human chimeric fuc
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41	622	31.6	342	15	AA19816315	Human alpha-1,3-fu
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44	580	29.4	342	18	AA19811820	Murine myeloid-lin
45	579	29.4	342	18	AA19826671	Mouse alpha-fucosy

ALIGNMENTS

RESULT 1
AA1980996
ID AA1980996 standard; Protein; 359 AA.
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XX
AC AA1980996;
XX
XX
DT 05-JUN-2000 (first entry)
XX
XX
DE Human alpha-1,3-fucosyltransferase.
XX
KW Alpha-1,3-fucosyltransferase; fucose; glycosylation; Lewis epitope;
KW brain; kidney; recombinant expression; transgenic animal; knockout
KW animal; FUC-TIV; drug screening; inhibitor; potentiator; diagnosis;
KW treatment; cancer; human.
XX
OS Homo sapiens.
XX
PN WO200006708-A1.
XX
PD 10-FEB-2000.
XX
PF 29-JUL-1999; 99WO-JP04092.
XX
PR 29-JUL-1998; 98JP-0213823.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Narimatsu H, Kudo T, Sasaki K;
XX
XX
DR WPI; 2000-183120/16.
DR N-PSDB; AA1982646, AA1982647.
XX
XX
PT Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
PT epitope and an antibody recognizing it useful for diagnosis of brain

PT and kidney disease and cancer. -
 PS Claim 2; Page 124-127; 172pp; Japanese.
 XX
 XX The invention relates to a novel alpha-1,3-fucosyltransferase which
 CC transfers a fucose moiety to galactosyl-beta-1-4-N-acetylglucosamine
 CC (generating the Lewis x or y epitope). It does not transfer a fucose
 CC moiety to alpha-2,3-sialyl-galactosyl-beta-1-4-N-acetylglucosamine
 CC and therefore does not generate the sialyl-Lewis x epitope. The
 CC invention also relates to DNA sequences encoding alpha-1,3-
 CC fucosyltransferase and expression vectors and host cells comprising these
 CC DNA sequences. The invention additionally encompasses the preparation of
 CC alpha-1,3-fucosyltransferase via the culture of transformed cells or by
 CC expression of the protein in a transgenic animal; antibodies which
 CC recognise alpha-1,3-fucosyltransferase; methods for screening potential
 CC inhibitors or potentiators of alpha-1,3-fucosyltransferase activity or
 CC expression; the preparation of compounds having fucose-containing sugar
 CC chains by use of the protein; and knockout non-human animals lacking
 CC alpha-1,3-fucosyltransferase. Alpha-1,3-fucosyltransferase has a similar
 CC substrate range to the known FUC-TIV and is expressed mainly in brain and
 CC kidney tissues. Alpha-1,3-fucosyltransferase, nucleotides which encode
 CC it, antibodies, potentiators and inhibitors may be used for the
 CC treatment and diagnosis of diseases of the brain and kidney, and of
 CC cancers. They may be used for the identification of substances
 CC which affect the activity or expression of alpha-1,3-fucosyltransferase;
 CC such substances may be used therapeutically. The knockout animals can
 CC be used to study the mechanisms of action and expression of alpha-1,3-
 CC fucosyltransferase. The present sequence represents human
 CC alpha-1,3-fucosyltransferase.
 XX
 SQ Sequence 359 AA;

Query Match 100.0%; Score 1970; DB 21; Length 359;
 Best Local Similarity 100.0%; Pred. No. 2e-170; Indels 0; Gaps 0;
 Matches 359; Conservative 0; Mismatches 0;
 QY 1 MTSTSGILRFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLKMKNFSTKTDY 60
 Db 1 MTSTSGILRFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLKMKNFSTKTDY 60
 QY 61 FNETTILVWVPPGQTFDLTSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 Db 61 FNETTILVWVPPGQTFDLTSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 QY 121 PQOARPPQKWIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPGFTVSTNPFVF 180
 Db 121 PQOARPPQKWIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPGFTVSTNPFVF 180
 QY 181 EVPSKEKLVCVVSNWNPENHARVYKYNELSKSIEIHTYGQAFGEYVNDKNIPTISACKF 240
 Db 181 EVPSKEKLVCVVSNWNPENHARVYKYNELSKSIEIHTYGQAFGEYVNDKNIPTISACKF 240
 QY 241 YLSFENSIIHKDYITEKLYNAPLAGSVPPVVLGSPSRENYENIPADSFIRVEDYNSPSLAK 300
 Db 241 YLSFENSIIHKDYITEKLYNAPLAGSVPPVVLGSPSRENYENIPADSFIRVEDYNSPSLAK 300
 QY 301 YLKEYDKNNKLYLSYFNWRKDTNVLPRFWSHACLDHVKRHOEYKSVGNLEKWFVN 359
 Db 301 YLKEYDKNNKLYLSYFNWRKDTNVLPRFWSHACLDHVKRHOEYKSVGNLEKWFVN 359

RESULT 2
 RAY80995
 ID AAY80995 standard; Protein; 359 AA.
 XX
 AC AAY80995;
 XX
 DT 05-JUN-2000 (first entry)
 XX Murine alpha-1,3-fucosyltransferase.
 DE
 XX Alpha-1,3-fucosyltransferase; fucose; glycosylation; Lewis epitope;
 KW brain; kidney; recombinant expression; transgenic animal; knockout

KW animal; FUC-TIV; drug screening; inhibitor; potentiator; diagnosis;
 KW treatment; cancer; murine; mouse.
 OS Mus sp.
 XX WO200006708-A1.
 XX
 PD 10-FEB-2000.
 XX
 XX 29-JUL-1999; 99WO-JP04092.
 PR 29-JUL-1998; 98JP-0213823.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Narimatsu H, Kudo T, Sasaki K;
 XX WPI; 2000-183120/16.
 DR N-PSDB; AA92645.
 XX
 PT Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
 PT epitope and an antibody recognizing it useful for diagnosis of brain
 PT and kidney disease and cancer.
 XX
 PS Claim 2; Page 121-124; 172pp; Japanese.
 XX
 CC The invention relates to a novel alpha-1,3-fucosyltransferase which
 CC transfers a fucose moiety to galactosyl-beta-1-4-N-acetylglucosamine
 CC (generating the Lewis x or y epitope). It does not transfer a fucose
 CC moiety to alpha-2,3-sialyl-galactosyl-beta-1-4-N-acetylglucosamine
 CC and therefore does not generate the sialyl-Lewis x epitope. The
 CC invention also relates to DNA sequences encoding alpha-1,3-
 CC fucosyltransferase and expression vectors and host cells comprising these
 CC DNA sequences. The invention additionally encompasses the preparation of
 CC alpha-1,3-fucosyltransferase via the culture of transformed cells or by
 CC expression of the protein in a transgenic animal; antibodies which
 CC recognise alpha-1,3-fucosyltransferase; methods for screening potential
 CC inhibitors or potentiators of alpha-1,3-fucosyltransferase activity or
 CC expression; the preparation of compounds having fucose-containing sugar
 CC chains by use of the protein; and knockout non-human animals lacking
 CC alpha-1,3-fucosyltransferase. Alpha-1,3-fucosyltransferase has a similar
 CC substrate range to the known FUC-TIV and is expressed mainly in brain and
 CC kidney tissues. Alpha-1,3-fucosyltransferase, nucleotides which encode
 CC it, antibodies, potentiators and inhibitors may be used for the
 CC treatment and diagnosis of diseases of the brain and kidney, and of
 CC cancers. They may be used for the identification of substances
 CC which affect the activity or expression of alpha-1,3-fucosyltransferase;
 CC such substances may be used therapeutically. The knockout animals can
 CC be used to study the mechanisms of action and expression of alpha-1,3-
 CC fucosyltransferase. The present sequence represents murine
 CC alpha-1,3-fucosyltransferase.
 XX
 SQ Sequence 359 AA;

Query Match 99.5%; Score 1961; DB 21; Length 359;
 Best Local Similarity 99.2%; Pred. No. 1.3e-169; Indels 0; Gaps 0;
 Matches 356; Conservative 2; Mismatches 1;
 QY 1 MTSTSGILRFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLKMKNFSTKTDY 60
 Db 1 MTSTSGILRFLIVCIILGCFMACLLIYIKPTNSWIFSPMESASSVLKMKNFSTKTDY 60
 QY 61 FNETTILVWVPPGQTFDLTSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 Db 61 FNETTILVWVPPGQTFDLTSCQAMFNIOGCHLTDRSLYNKSHAVLIHHRDISWDLTNL 120
 QY 121 PQOARPPQKWIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPGFTVSTNPFVF 180
 Db 121 PQOARPPQKWIWMNLESPTHTPKSGIEHLFNLTLTYRRSDIQVPGFTVSTNPFVF 180
 QY 181 EVPSKEKLVCVVSNWNPENHARVYKYNELSKSIEIHTYGQAFGEYVNDKNIPTISACKF 240
 Db 181 EVPSKEKLVCVVSNWNPENHARVYKYNELSKSIEIHTYGQAFGEYVNDKNIPTISACKF 240

```
Query Match          35.08; Score 689.5; DB 12; Length 405;
Best Local Similarity 38.5%; Pred. No. 4.5e-54;
Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;
```

```
Qy      15 VCIIILGCFMAC--LLIYI----KPTNSWISPMESASSVLKKMKNFSTKTDFYNETITLV 68  
       |||:         |   |   |   |  
Db      28 VCVLAAAGLTCTALITVACWGOLPLPWA-SPTSS-----RPVGILL 68
```


CC It was decoded from the appropriate cDNA. The method of the invention
 CC is used to produce membrane-bound mammalian glycosyltransferase and
 CC variants, using transformed yeasts. It is less time consuming than
 CC natural source isolation and chemical methods.

XX SQ Sequence 405 AA;

Query Match 35.0%; Score 689.5; DB 13; Length 405;

Best Local Similarity 38.5%; Pred. No. 4.5e-54;

Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI---KPTNSWIFSPMESASSVLKMKNFFSTKTDYFNETTILV 68

Db 28 VCVLAAGLCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68

QY 69 WVPFPGQTDL---TSCQAMFIQGHLLTDRSLYNKSHAVLIHHRDI-----SW---- 115

Db 69 WVPFPGGRDSAPRPPDCRLRNFISGCRLLTDRASYGEOAVLFHHRDLVKGPDPWPPW 128

QY 116 -----DLNLPQO-----ARPPFOKIWMNLESPTHTP-QKSGIEHL 151

Db 129 GIOAHTAEVDLRYLDYEEAAAALATSPRPPGQRYWMMNFESPSGLRSLASNL 188

QY 152 FNLTLYRRSDIQVPYGFVTSTNPFVEVPS-----KEKLVCMVSYNNPEHARV 203

Db 189 FNTWLSYRSDVFPYGYLYPRSH--GPPSGLAPPLSRKQGLVAVVYSHWDERQARV 246

QY 204 KYNELSKSIEIHTYGOAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261

Db 247 RYHQLSQHVTVDVFGRGPGQPVPPEIGLHTVARYKYLAFENSQHLDYITEKLWNLAL 306

QY 262 LAGSVPVVLGSPRENYENYIPADSFHVEDYNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321

Db 307 LAGAVPVVLGPDNRANYERFVRGAFIHVDDFPSASSLASYLLEFLDRNPVAVRYRFFHWR 366

QY 322 FTVNLPWFESHACLADHKRHOEY-KSVGNLEKWF 357

Db 367 YAVHITSFWDPEWPCRVQAVQVORAGDRPKSRINLASWF 403

RESULT 7

AAR14405

ID AAR14405 standard; Protein; 530 AA.

XX AC AAR14405;

XX 13-FEB-1992 (first entry)

XX Protein 1 (1.3-fucosyl transferase).

XX CDX; cell adhesion; ELAMI.

XX Homo sapiens.

XX WO9116900-A.

XX 14-NOV-1991.

XX 26-OCT-1990; 90WO-US06198.

XX 27-APR-1990; 90WO-US02357.

XX 26-OCT-1990; 90WO-US06198.

XX (BIO) BIOGEN INC.

XX Goelz SE, Hession CA;

XX WPI; 1991-353507/48.

XX N-PSDB; AAQ14383.

XX DNA sequences encoding 1,3-fucosyl transferase - used to develop

XX antiinflammatory therapy by inhibition of linking activity.

PS Claim 23; Fig 2; 38pp; English.

XX The sequence was deduced from CDX pCDM8 clone 1. The protein, a 1,3-
 CC fucosyl transferase is a surface glycoprotein which is recognised by
 CC anti-CDX antibodies and which binds to ELAM1. The portion of the
 CC sequence from 126-530 is identical to protein 7.2 (encoded by clone
 CC 7.2; AAQ14382). The two proteins may represent different transcripts
 CC from the same DNA segment. The protein may be useful in the development
 CC of anti-inflammatory or other therapies.
 CC See also AAR14404.

XX SQ Sequence 530 AA;

Query Match 35.0%; Score 689.5; DB 12; Length 530;

Best Local Similarity 38.5%; Pred. No. 6.5e-54;

Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI---KPTNSWIFSPMESASSVLKMKNFFSTKTDYFNETTILV 68

Db 153 VCVLAAGLCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 193

QY 69 WVPFPGQTDL---TSCQAMFIQGHLLTDRSLYNKSHAVLIHHRDI-----SW---- 115

Db 194 WVPFPGGRDSAPRPPDCRLRNFISGCRLLTDRASYGEOAVLFHHRDLVKGPDPWPPW 253

QY 116 -----DLNLPQO-----ARPPFOKIWMNLESPTHTP-QKSGIEHL 151

Db 254 GIOAHTAEVDLRYLDYEEAAAALATSPRPPGQRYWMMNFESPSGLRSLASNL 313

QY 152 FNLTLYRRSDIQVPYGFVTSTNPFVEVPS-----KEKLVCMVSYNNPEHARV 203

Db 314 FNTWLSYRSDVFPYGYLYPRSH--GPPSGLAPPLSRKQGLVAVVYSHWDERQARV 371

QY 204 KYNELSKSIEIHTYGOAF-GEYVNDKNLIPTISACKFYLSFENSIIHKDYITEKLY-NAF 261

Db 372 RYHQLSQHVTVDVFGRGPGQPVPPEIGLHTVARYKYLAFENSQHLDYITEKLWNLAL 431

QY 262 LAGSVPVVLGSPRENYENYIPADSFHVEDYNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321

Db 432 LAGAVPVVLGPDNRANYERFVRGAFIHVDDFPSASSLASYLLEFLDRNPVAVRYRFFHWR 491

QY 322 FTVNLPWFESHACLADHKRHOEY-KSVGNLEKWF 357

Db 492 YAVHITSFWDPEWPCRVQAVQVORAGDRPKSRINLASWF 528

RESULT 8

AAR45937

ID AAR45937 standard; Protein; 405 AA.

XX AC AAR45937;

XX 26-JUL-1994 (first entry)

XX A glycosyltransferase.

XX Glycosyltransferase; fucosyltransferase; GDP-Fuc; in vitro; cell;

XX surface; oligosaccharide.

XX Homo sapiens.

XX WO9402616-A.

XX 03-FEB-1994.

XX 20-JUL-1993; 93WO-US06703.

XX 20-JUL-1992; 92US-0914281.

XX (UNMI) UNIV MICHIGAN.

XX Lowe JB;

XX

DR WPI: 1994-048874/06.
DR N-PSDB: AAQ56909.

PT DNA fragment encoding a glycosyltransferase - can be used for in
PT vitro reactions to modify cell surface oligosaccharide(s) e.g.
PT blood gp. determinants, to protect against transplant rejection

XX Disclousure; Fig 4; 249pp; English.

XX The sequence is that of a human glycosyl transferase. The enzyme
CC may be non glycosylated. This prevents premature loss of enzyme
CC activity. It can also be used in in vitro reactions to modify cell
CC surface oligosaccharide mols. e.g. blood group determinants.
CC See also AAR45933-9.

XX Sequence 405 AA;

Query Match 34.8%; Score 685.5; DB 15; Length 405;

Best Local Similarity 38.5%; Pred. No. 1e-53; Indels 75; Gaps 14;

Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETTILV 68

DB 28 VCVLAAAGLTCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68

QY 69 WWPFGQTFDL-----TSCQAMFNIGQCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115

DB 69 WWPFGGRDSAPRPPDCPLRFNISGCRLLTDRASYGQAQVLFHHRDLVKGPPDPPPW 128

QY 116 -----DLTNLPOQ-----ARPPFQKIWMNLESPTHTP-QKSGIEHL 151

DB 129 GIOAHTAEVDRLVDYEAAAAEALATSSPRPPGQWVWVNFESPSHSPGLRLSLASNL 188

QY 152 FNLTLYRRSDIQVPGFLVSTNPFVFEVPS-----KEKLVCMVWVNNWNPHEARV 203

DB 189 FNWTLSTRADSDVFPYGYLYPRSHP--GDPFSGLAPPLSRKQGLVAVVSHWDDROARV 246

QY 204 KYNELSKSIEHTYGOAF-GEYVNDKNLPTISACKFYLSFENSIIKDYITEKLY-NAF 261

DB 247 RYHOLSQHVTVDFEGCGPGQVPEIGLLHTVARYKFLAFENSQHLDTYITEKLWRNAL 306

QY 262 LAGSPVVLGSPRENYENIPADSFHVEDYNSPELAKYLKEVDKNNKLYLSYFNMRKD 321

DB 307 LAGAPVVLGPDRAVYAFVPRGAFIHVDVDFPSASSLASYLFLDRNPVARYRYFHWRRS 366

QY 322 FTVNLPRFRESHACLADCHVKRHOEY-KSVGNLEKWF 357

DB 367 YAVHITSFWEDEPWCRCVQAVQAGDRPKSIRNLASWF 403

RESULT 9

AAWI13641 standard; Protein; 405 AA.

XX AC AAW13641;

XX DT 19-JUN-1997 (first entry)

XX Human alpha(1,3)-fucosyltransferase (Fuc-TIV).

XX Alpha(1,3)-fucosyltransferase; Lewis enzyme; Fuc-TIV;

XX glycosylation; oligosaccharide; blood group.

XX OS Homo sapiens.

XX PN WO9709421-A1.

XX PD 13-MAR-1997.

XX PF 06-SEP-1996; 96WO-US13816.

XX PR 08-SEP-1995; 95US-0525058.

XX

PA (UNMI) UNIV MICHIGAN.

XX Legault DJ, Lowe JB;

XX WPI; 1997-192897/17.

XX DR N-PSDB; AAT61678.

XX New recombinant fucosyltransferase proteins - useful for modifying
PT cell surface oligosaccharide structures

XX Example 4; Page 284-285; 329pp; English.

XX Human GDP-Fuc-beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)-fucosyltransferase

CC (Fuc-TIV) (AAW13641) can utilize type II acceptor substrates, but not

CC type I substrates, and therefore cannot form the sialyl Lewis x

CC determinant. amino acid sequence was deduced from an isolated

CC DNA sequence obtained from a human genomic DNA using Lewis enzyme cDNA

CC (see also AAT61675) as probe. the fuc-TIV enzyme, when expressed by

CC de novo expression of specific cell surface glycoconjugate structures

CC that are recognised by antibodies against SSEA-1 or Lewis x and by an

CC antibody against the VIM-2 determinant.

XX Sequence 405 AA;

Query Match 34.8%; Score 685.5; DB 18; Length 405;

Best Local Similarity 38.5%; Pred. No. 1e-53;

Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETTILV 68

DB 28 VCVLAAAGLTCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68

QY 69 WWPFGQTFDL-----TSCQAMFNIGQCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115

DB 69 WWPFGGRDSAPRPPDCPLRFNISGCRLLTDRASYGQAQVLFHHRDLVKGPPDPPPW 128

QY 116 -----DLTNLPOQ-----ARPPFQKIWMNLESPTHTP-QKSGIEHL 151

DB 129 GIOAHTAEVDRLVDYEAAAAEALATSSPRPPGQWVWVNFESPSHSPGLRLSLASNL 188

QY 152 FNLTLYRRSDIQVPGFLVSTNPFVFEVPS-----KEKLVCMVWVNNWNPHEARV 203

DB 189 FNWTLSTRADSDVFPYGYLYPRSHP--GDPFSGLAPPLSRKQGLVAVVSHWDDROARV 246

QY 204 KYNELSKSIEHTYGOAF-GEYVNDKNLPTISACKFYLSFENSIIKDYITEKLY-NAF 261

DB 247 RYHOLSQHVTVDFEGCGPGQVPEIGLLHTVARYKFLAFENSQHLDTYITEKLWRNAL 306

QY 262 LAGSPVVLGSPRENYENIPADSFHVEDYNSPELAKYLKEVDKNNKLYLSYFNMRKD 321

DB 307 LAGAPVVLGPDRAVYAFVPRGAFIHVDVDFPSASSLASYLFLDRNPVARYRYFHWRRS 366

QY 322 FTVNLPRFRESHACLADCHVKRHOEY-KSVGNLEKWF 357

DB 367 YAVHITSFWEDEPWCRCVQAVQAGDRPKSIRNLASWF 403

RESULT 10

AAWI1821

ID AAW11821 standard; Protein; 405 AA.

XX AC AAW11821;

XX DT 06-MAY-1997 (first entry)

XX Human myeloid derived fucosyltransferase (FUC-TIV).

XX Fucosyltransferase; FUC-TIV; fucosylation; antibody; IgG; Igm;

XX septic shock; septicemia; therapy.

XX OS Homo sapiens.


```
PN WO9640881-A1.
XX
PD 19-DEC-1996.
XX
XX 08-MAY-1996; 96WO-US06427.
XX
XX 07-JUN-1995; 95US-0483151.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Holgersson J, Seed B;
XX
XX WPI: 1997-108639/10.
DR N-PSDB; AAT58506.
XX
XX New murine alpha-(1,3)-fucosyltransferase - for fucosylating an
PT antibody to protect mammals against e.g. septic shock or septicaemia
XX
XX Claim 17; Fig 6B; 58pp; English.
XX
XX Introduction of human myeloid cell-specific fucosyltransferase
CC Fuc-TIV (AAW11821) into a murine cell line results in the appearance
CC of a fucosylated glycan pattern similar to that found on human
CC neutrophils and monocytes. Murine cells expressing human Fuc-TIV
CC show enhanced adhesion to E-selectin fusion proteins, indicating
CC that Fuc-TIV is involved in human granulocyte extravasation. Host
CC cells (e.g. 32D c13 or human 293 cells) transformed with DNA (see
CC also AAT59506) encoding Fuc-TIV and DNA encoding murine alpha-(1,3)-
CC fucosyltransferase (see also AAW11820), can be used to fucosylate
CC ADP-antibody, IgG or IgM for use in protecting an animal against an
CC adverse immune reaction, esp. septic shock or septicaemia.
XX
XX Sequence 405 AA;
XX
XX Query Match 34.6%; Score 681.5; DB 18; Length 405;
XX Best Local Similarity 38.0%; Pred. No. 2.4e-53;
XX Matches 151; Conservative 61; Mismatches 110; Indels 75; Gaps 14;
XX
XX QY 15 VCIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKYDYNETTILV 68
XX Db 28 VCVLAAAGLCTALITYACWGLPLPFWA-SPTPS-----RPGVLL 68
XX
XX QY 69 WWPFGQTEDL---TSCQAMENIOGCHLTDRSLYNKSHAVLIHHRDI-----SW---- 115
XX Db 69 WWPFGGAISAPRPDPDCRLRFNLSGCRLLTDRASYGAQAVLFHHDLVKGPPDPWPPW 128
XX
XX QY 116 -----DLTNLPQO-----ARPPFQKWIWMNLESPTHTP-QKSGIEHL 151
XX Db 129 GIGAHTAEVDLRLDYEEAAAAEALATSSPRPRAKRWYWMNFESPSHGLRSLASNL 188
XX
XX QY 152 FNLTLYRRSDIQVYGFIVTSTNPFVEVPS-----KKLVGVVYVSNWNPHEARY 203
XX Db 189 FNNWLSYRADSDVFPVGYLYPRSH--GDPPSGLAPPLSRKQGLVAVVYSHWDERQARV 246
XX
XX QY 204 KYNELSKSTEIHTYGQAF-GEVYNDKNLPTISACKFYLSEFNSIHKDYITEKLY-NAF 261
XX Db 247 RYTHQLSQHTVDVFGGCGQVPELGLLHTVARYKFYLAFENSQHLDTYTEKLMRNAL 306
XX
XX QY 262 LAGSVPVVLGPSRENYENIYPADSFTHVEDYNSPSELAKYLKEVDKNNKILYLFYNNRKD 321
XX Db 307 LAGAVPVVLGPDRAHYERFYPGAFIHVDVDFPSASSLASLYLLDLDRNPAYRYRFFHRRS 366
XX
XX QY 322 FTVNLPRFESHACLADHKVHRQEV-KSVGNLEKWF 357
XX Db 367 YAVHITSFDEPWCRCQAVQVRAGDRPKSRNLASWF 403
XX
XX RESULT 11
XX AAW14515
XX ID AAW14515 standard; Protein; 360 AA.
XX
XX AC AAW14515;
XX
XX
```

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DT 19-JUN-1997 (first entry)
XX
DE Human chimeric fucosyltransferase Fuc-TC4.
XX
XX Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC4.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..159
FT /label= Fuc-TIV
FT /note= "amino acids 1-159 of Fuc-TIV"
FT 160..360
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT 46
FT /label= Glycosylation
FT 91
FT /label= Glycosylation
FT 153
FT /label= Glycosylation
XX
XX WO9709421-A1.
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX
XX WPI: 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
XX Claim 1; Refer to Page 294; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX (AAT61675, AAT61680) and expression in transformed host cells. The
XX chimeric fucosyltransferases can be used to modify cell surface
XX oligosaccharide structures.
XX
XX Sequence 360 AA;
XX
XX Query Match 34.3%; Score 676; DB 18; Length 360;
XX Best Local Similarity 42.8%; Pred. No. 6.3e-53;
XX Matches 133; Conservative 62; Mismatches 104; Indels 12; Gaps 8;
XX
XX QY 55 STDTDFNERTILVWVPFGQTEDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
XX Db 53 STGTPAHSIPLILLWVFPFKPIALPCSEWPGTADCNITADRKVTPQADAVIHREV 112
XX
XX QY 114-SWD-LTNLPQOARPPFQKWIWMNLESPTHTPQKSGIEHLENLTLYRRSDIQVYGFILT 172
XX Db 113 MYNPSAQLPSRPRQGRWIWFSMESPSHCWQLKAMDGYENLWMSYRSDSDITTPYGLWE 172
XX
XX QY 173 V-STNPF--VFVEPSKEKLVGVVYVSNWNPHEARKYKYNELSKSIEIHTYGQAFGEVYNDK 229
XX Db 173 PWSGQPAHPPLNLNAKTELVAWAVSNWKPDSARVRYQSLQAHLKVDVYGRSH-KLPLKG 231
XX
XX QY 230 NLIPTISACKFYLSEFNSIHKDYITEKLY-NAFLASVVPVVLGPSRENYENIYPADSFH 288
XX
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Db 232 TMMETLSRYKFYLAENSLHPDYITEKLRNALNAEAWPVVVLGSPRSNRYERFLPPDAFIH 291
QY 289 VEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKDFVNLPR--FWESHACACLDHVKRHOE 346
Db 292 VDDFQSPKDLARYLQELDKDHARYLSYFWRWRETLR---PRFSWALDFCKACWKLOQESR 348
QY 347 YKSVGNLEKWF 357
Db 349 YQTVRSIAAWF 359

RESULT 12
AAW14514
ID AAW14514 standard; Protein; 360 AA.
AC AAW14514;
XX
XX
DT 19-JUN-1997 (first entry)
DE Human chimeric fucosyltransferase Fuc-TC3.
XX
XX Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC3.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..300
FT /label= Fuc-TIV
FT /note= "amino acids 1-300 of Fuc-TIV"
FT Region 301..360
FT /label= Fuc-TIII
FT /note= "amino acids 302-361 of Fuc-TIII"
FT Modified-site 46
FT /label= Glycosylation
FT Modified-site 91
FT /label= Glycosylation
FT Modified-site 153
FT /label= Glycosylation
FT
FT
XX WO9709421-A1.
PN
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
XX Claim 1; Refer to Page 294; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX GlcNAc(GlcNAc alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX (AAW161675, AAW161680) and expression in transformed host cells. The
XX chimeric fucosyltransferases can be used to modify cell surface
XX oligosaccharide structures.
XX
XX Sequence 360 AA;

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Query Match 34.3%; Score 675; DB 18; Length 360;

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Best Local Similarity 42.8%; Pred. No. 7.8e-53;
Matches 133; Conservative
QY 55 STKTDYFNEITILVWVPFGOTFDLTSCQAMP-NIOGCHLTTRDSLYNKSHAVLIHHRDI 113
Db 53 STGTPAHSIPILLLWTFNFKPIALPRCSEMPVPGTADCNITADRKVYPQADAVIVHREV 112
QY 114 SWD-LTNLPQOARPPFOKWIWMNLESPTHIPQKSGIEHLNLTLYRRDSIQVPGFLT 172
Db 113 MYNPSAQLPRSPRQGRWIWFSMESPSHCWQLKAMDGYFNLTMSYRSDSDITFTYGWLE 172
QY 173 V-STNPF--VFEPVSEKLYCVVSVNNWNPHEARVYKYYNELSKSIEHTHYGOAFGEYVNDK 229
Db 173 PWSGQPAHPPLNLISAKTELVAWAVSNMGPSARVRYYSQSLQAHLKVDVYGRSH-KPLPQG 231
QY 230 NLIPTISACKFYLSFENSIIHKDYITEKLY-NAFLAGSVPPVVLGSPRSNRYENYIPADSFIH 288
Db 232 TMMETLSRYKFYLAENSLHPDYITEKLRNALNAEAWPVVVLGSPRSNRYERFLPPDAFIH 291
QY 289 VEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKDFVNLPR--FWESHACACLDHVKRHOE 346
Db 292 VDDFQSPKDLARYLQELDKDHARYLSYFWRWRETLR---PRFSWALDFCKACWKLOQESR 348
QY 347 YKSVGNLEKWF 357
Db 349 YQTVRSIAAWF 359

RESULT 13
AAW14530
ID AAW14530 standard; Protein; 361 AA.
XX
XX AAW14530;
XX
XX 19-JUN-1997 (first entry)
XX
XX Human chimeric fucosyltransferase Fuc-TC19.
XX
XX Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC19.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..99
FT /label= Fuc-TIII
FT /note= "amino acids 1-99 of Fuc-TIII"
FT Region 100..160
FT /label= Fuc-TVI
FT /note= "amino acids 99-159 of Fuc-TVI"
FT Region 161..361
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT Modified-site 154
FT /label= Glycosylation
XX
XX WO9709421-A1.
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures

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XX PS Claim 1; Refer to Page 298; 329pp; English.
XX PS
XX CC Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX CC comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX CC GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIIII, Lewis
XX CC enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX CC GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX CC obtd. by cassette mutagenesis of Fuc-TIIII and Fuc-TVI nucleic acids
XX CC (AAT61675, AAT61680) and expression in transformed host cells. The
XX CC chimeric fucosyltransferases can be used to modify cell surface
XX CC oligosaccharide structures.
XX PS Sequence 361 AA;

Query Match 34.2%; Score 674; DB 18; Length 361;
Best Local Similarity 43.7%; Pred. No. 9.7e-53;
Matches 131; Conservative 60; Mismatches 97; Indels 12; Gaps 8;

QY 66 ILVWVPPGQTFDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQQ 123
Db 65 ILLWTWPFHPIPVALSRCSEMPGTADCHITADRKVPQADTVVHHREVNYNPSAQLPRS 124
QY 124 ARPPFOKIWMNLESPTHTPKSGIEHLFNLTITRYRDSDIQVPGFLTV-STNPF--VF 180
Db 125 PRQQQEWIWFESHSCHQKAMDGYFNLTMSYRSDSDIFTYPGWLEPWSQPAHPPL 184
QY 181 EVPSKEKLVYCWVYNNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTISACKF 240
Db 185 NLSAKTELAVAWSNWPKPDSARVYQSLQAHKLVGVGRSH-KPLPKGTMMETLSRYKF 243
QY 241 YLSFENSIHKDYITEKLY-NAFLAGSVVPVVLGSPRENYENIYPADSFIVHEDYNSSELA 299
Db 244 YLAFENSLHPDYITEKLWRNALEAWAVPVVVLGSPRSNYERFLPPDAFIVHDDFQSPKDLA 303
QY 300 KYLKEVDKNNKLYSYFNWRKDFTVNLP--FWESHACLACDHVKRHOEYKSVGNLEKWF 357
Db 304 RYLQELDKDHARYLSYFRWRETLR---PRSFWSALDFCKACWKLOQESRYQTVRISIAAWF 360

RESULT 14
AAW14520
ID AAW14520 standard; Protein; 361 AA.
XX AC AAW14520;
XX AC AAW14520;
XX DT 19-JUN-1997 (first entry)
XX DE Human chimeric fucosyltransferase Fuc-TC9.
XX KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIIII;
XX KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
XX KW oligosaccharide; Fuc-TC9.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT Region 1..130
XX FT /label= Fuc-TIIII
XX FT /note= "amino acids 1-130 of Fuc-TIIII"
XX FT Region 131..160
XX FT /label= Fuc-TVI
XX FT /note= "amino acids 130-159 of Fuc-TVI"
XX FT Region 161..361
XX FT /label= Fuc-TIIII
XX FT /note= "amino acids 161-361 of Fuc-TIIII"
XX FT Modified-site 154
XX FT /label= Glycosylation
XX PN WO9709421-A1.
XX PD 13-MAR-1997.
XX PS

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PF 06-SEP-1996; 96WO-US13816.
XX PR 08-SEP-1995; 95US-0525058.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Legault DJ, Lowe JB;
XX WI 1997-192897/17.
XX DR WPI;
XX PT New recombinant fucosyltransferase proteins - useful for modifying
XX PT cell surface oligosaccharide structures
XX PS Claim 1; Refer to Page 295; 329pp; English.
XX PS
XX CC Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX CC comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX CC GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIIII, Lewis
XX CC enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
XX CC GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX CC obtd. by cassette mutagenesis of Fuc-TIIII and Fuc-TVI nucleic acids
XX CC (AAT61675, AAT61680) and expression in transformed host cells. The
XX CC chimeric fucosyltransferases can be used to modify cell surface
XX CC oligosaccharide structures.
XX PS Sequence 361 AA;

Query Match 34.2%; Score 673; DB 18; Length 361;
Best Local Similarity 43.4%; Pred. No. 1.2e-52;
Matches 132; Conservative 57; Mismatches 95; Indels 20; Gaps 9;

QY 66 ILVWVPPGQTFDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
Db 65 ILLWTWPFHPIPVALSRCSEMPGTADCHITADRKVPQADTVVHH---WDIMSNPKSR 120
QY 120 LPQAAAPPPFOKIWMNLESPTHTPKSGIEHLFNLTITRYRDSDIQVPGFLTV-STNPF 178
Db 121 LPSPRPQGGQWLVFESHSCHQKAMDGYFNLTMSYRSDSDIFTYPGWLEPWSQPA 180
QY 179 --VFEVPSKEKLVYCWVYNNWNNPEHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLIPTIS 236
Db 181 HPPNLNSAKTELAVAWSNWPKPDSARVYQSLQAHKLVGVGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSFENSIHKDYITEKLY-NAFLAGSVVPVVLGSPRENYENIYPADSFIVHEDYNSP 295
Db 240 RYKFLAFENSLHPDYITEKLWRNALEAWAVPVVVLGSPRSNYERFLPPDAFIVHDDFQSP 299
QY 296 SELAKYLKEVDKNNKLYSYFNWRKDFTVNLP--FWESHACLACDHVKRHOEYKSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRSFWSALDFCKACWKLOQESRYQTVRIS 356
QY 354 EKWF 357
Db 357 AAWF 360

RESULT 15
AAW14517
ID AAW14517 standard; Protein; 361 AA.
XX AC AAW14517;
XX AC AAW14517;
XX DT 19-JUN-1997 (first entry)
XX DE Human chimeric fucosyltransferase Fuc-TC6.
XX KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIIII;
XX KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
XX KW oligosaccharide; Fuc-TC6.
XX OS Synthetic.
XX FT Key Location/Qualifiers

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FT	Region	1..70	/label= Fuc-TIIII
FT		/note= "amino acids 1-70 of Fuc-TIIII"	
FT	Region	71..86	/label= Fuc-TVI
FT		/note= "amino acids 70-85 of Fuc-TVI"	
FT	Region	87..361	/label= Fuc-TIIII
FT		/note= "amino acids 87-361 of Fuc-TIIII"	
FT	Modified-site	154	/label= Glycosylation
FT			

13-MAR-1997.

08-SEP-1995: 95US-0525058.

XX
PI Legault DJ. Lowe JB:

XX
DR WPT: 1997-192897/17

XX
PT
New recombinant fucXX
FT cell surface oligosac

PS Claim 1; Refer to page 295; 329pp; English.
XX

CC
chimeric fucosyltran-
comprise portions of

CC CC GlnNAc(Glc) alpha(1,3)/1,4)-fucosyltransferase (Fuc-TII), Lewis
CC enzyme) (AAW13638) and portions of the GDP-Fuc-D-Gal-(1,4)-D-
CC CC GlcNAc alpha(1,3)fucosyltransferase (Fuc-TV) (AAW13643). They are
CC CC obtd by cassette mutagenesis of Fuc-TIII and Fuc-TV nucleic acids
CC (AM161675, AM161680) and expression in transformed host cells. The
CC chimeric fucosyltransferases can be used to modify cell surface
CC oligosaccharide structures.

AA	Sequence	361 AA:
SO		

Query Match	34.1%	Score 672;	DB 18;	Length 361;
Best Local Similarity	43.1%;	pred. No. 1.5e-52;		
Matches 131; Conservative	55;	Mismatches 98;	Indels 20;	Gaps 9;

QY 66 ILVWWPFGQTFDLTSCQAMF-NIQGCHLTTRSLYNKSHAVLIHHRDISWDL-----TN 119

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APPENDIX

Search completed: October 8, 2002, 16:52:17

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 16:34:47 ; Search time 15.5 Seconds
(without alignments)
2225.553 Million cell updates/sec

Title: US-09-744-748-2

Perfect score: 1970

Sequence: 1 MWTSGILRPFLIVCIILG.....HVKRHOEYKSVGNLEKWFVN 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	703	35.7	433	2 A57596	alpha-1,3-fucosyl
2	695	35.3	400	2 JC4591	alpha-1,3 fucosyl
3	689.5	35.0	405	2 B36340	alpha(1,3)-fucosyl
4	667	33.9	361	2 A36669	galactoside 3(4)-L
5	667	33.9	374	2 A42270	alpha (1,3) fucosyl
6	662.5	33.6	359	2 A45156	alpha-(1,3)-fucosyl
7	653	33.1	365	2 S55498	alpha(1,3/4)-fucosyl
8	647	32.8	364	2 I39048	alpha (1,3) fucosyl
9	619	31.4	342	2 A54057	alpha(1,3) fucosyl
10	478.5	24.3	304	2 I39049	alpha (1,3) fucosyl
11	311	15.8	414	2 T15270	hypothetical prote
12	308	15.6	1652	2 T16799	hypothetical prote
13	281.5	14.3	451	2 T23491	hypothetical prote
14	224.5	11.4	393	2 H96742	hypothetical prote
15	203.5	10.3	513	2 F96533	probable fucosyltr
16	160.5	8.1	183	2 C97832	alpha-(1,3)-fucosyl
17	151.5	7.7	346	2 T44327	hypothetical prote
18	131	6.6	436	2 G71862	alpha-(1,3)-fucosyl
19	129.5	6.6	425	2 C64567	fucosyltransferase
20	129	6.5	454	2 B71914	alpha (1,3)-fucosyl
21	128.5	6.5	476	2 C64601	fucosyltransferase
22	123.5	6.3	876	2 S71277	serine/threonine-s
23	123.5	6.3	876	2 D85350	hypothetical prote
24	112.5	5.7	682	2 F81332	probable periplasm
25	110	5.6	1088	2 T41671	hypothetical prote
26	105.5	5.4	789	2 G90587	lipoprotein [impor
27	105	5.3	537	2 T21823	hypothetical prote
28	103	5.2	747	2 T33488	hypothetical prote
29	102	5.2	2628	2 S59413	probable membrane

30	101.5	5.2	354	2 B97003	spermidine/putresc
31	101	5.1	4550	2 T18440	hypothetical prote
32	100.5	5.1	382	2 T29554	hypothetical prote
33	99.5	5.1	335	2 AD1880	hypothetical prote
34	99.5	5.1	759	2 I38593	fibroblast activat
35	99	5.0	526	2 J82873	hypothetical prote
36	98.5	5.0	781	1 Q08B7	helicase (EC 3.6.1
37	98	5.0	392	2 D64433	hypothetical prote
38	98	5.0	408	2 T47585	hypothetical prote
39	98	5.0	441	2 F84560	purple acid phosph
40	96	4.9	387	2 JC2484	xylan endo-1,3-bet
41	96	4.9	566	2 JH0218	cellulase (EC 3.2.
42	96	4.9	2059	2 T41933	large tegument pro
43	95.5	4.8	340	2 T46112	hypothetical prote
44	95.5	4.8	370	2 JC7591	spinal cord-derive
45	95.5	4.8	373	2 F81438	probable periplasm

ALIGNMENTS

RESULT 1

A57596

alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - mouse

N:Alternate names: ELAM-1 ligand fucosyltransferase homolog

C:Species: Mus musculus (house mouse)

C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 11-Jan-2000

C:Accession: A57596

R:Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.,

J. Biol. Chem. 270, 25047-25056, 1995

A:Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific e

rase.

A:Reference number: A57596; MUID:96027607

A:Accession: A57596

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-433 <R>

C:Cross-references: GB:033457; NID:gl039426; PIDN:AAC52269.1; PID:gl039427

C:Superfamily: galactoside 3(4)-L-fucosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 35.7%; Score 703; DB 2; Length 433;
Best Local Similarity 42.4%; Pred. No. 4.9e-46;
Matches 145; Conservative 49; Mismatches 96; Indels 52; Gaps 8;

QY 66 ILVWVWPF-----GQTDLTSCQAMFNIGQCHLTDRSLYKSHAVLIHHRDISMDLTNLP 121

Db 92 VLLWWEFGRGGYKPKSPDCSLRFNISGCRLLTDRAAYGEAQAVLFHRDLVKELHWP 151

QY 122 QQ-----ARPPFQKWMNLESPTHTPKSG 147

Db 152 PMGARERTKALVLRVDDQEGAVTLTGKALETVGSRPPGQRMWNNFESPSHTPLRG 211

QY 148 I-EHLPLTLTYRRDSIOQYGYPLTVSTNPFVPEVPS-----KEKLCVWVSWNWP 198

Db 212 LAKDLFWNTLSYRTDSVDFPYGLYSRSDP--TEQSGGLGQPQARGLVWVWVSWNNE 269

QY 199 EHARKYNNELSKSIEHTYQCAF-GEYVNDKNLIPTISACKFYLSFENSITKDYIEKL 257

Db 270 HQARVRYHQLSRHVSVDVFGRTGPRVPAIGLLHTVARYKYFLAFENSRHVDYIEKL 329

QY 258 Y-NAFLAGSPVVLGSPRENYIPADSIHVEDYNSPSELAKYLKEVDKNNKLYSYF 316

Db 330 WRNLAAGAPVVLGPDPRANYERFVPRGAFIHVDDFFNAASLAAYLLFLDRNVAVRYRF 389

QY 317 NWRKDTVNLPRWESHACLACDHVKRH-QEYKSVGNLEKWF 357

Db 390 RWRRSFAVHITSFWEQWCRTCQAVQSGDQPKSIHNLADWF 431

RESULT 2

JC4591

alpha-1,3 fucosyltransferase (EC 2.4.1.-) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
C:Accession: J04591
R:Ozawa, M.; Muramatsu, T.
J. Biochem. 119, 302-308, 1996
A:Title: Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene
A:Reference number: J04591; MUID:97037075
A:Accession: J04591
A:Molecule type: mRNA
A:Residues: 1-400 <OZ>
A:Cross-references: DBJ:D63379
A:Experimental source: Embryonal carcinoma F9 cells
C:Keywords: galactoside 3(4)-L-fucosyltransferase; hexosyltransferase
F:1-23/Domain: intracellular #status predicted <INT>
F:24-49/Domain: transmembrane #status predicted <TRM>
F:84,185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.3%; Score 695; DB 2; Length 400;
Best Local Similarity 41.8%; Pred. No. 1.8e-45;
Matches 143; Conservative 51; Mismatches 96; Indels 52; Gaps 8;

QY 66 ILVWVWF-----GQFDLTSCQAMNIOGCHLTDRSLYNKSHAVLIHHRDLSWDLTNLP 121
DB 59 VLLWEPFGRGGYKSPDPCSLRNISGCRLLTDRAAYGEAAQVLFHHRDLVKKELHWP 118
QY 122 QQ-----ARPPQKVIWMNLESPHTHPQKSG 147
DB 119 PPGARERTDKALVLRVDDQEGAVTLGKALETVGSRPPGQRYWMNFSPSHTPGLRG 178
QY 148 I-EHLNLTATYRRSDIOVPYGLFTVSTNPFVFPVS-----KEKLVGVYVNNWNP 198
DB 179 LAKDLNFWTLSTYRSDVFPVGYLSRSDP--TEQPSGLGAPPLARKOGLEAWVYVNNNE 236
QY 199 EHARKYNNELSKSIETIHYGQAF-GEVYNDKNLIPTISACKFYLSFENSISKDKYITEKL 257
DB 237 HQAQVRYXHQLSRHVSVDVFGRTGPRVPVPAIGLLHTVARYKFLAFENSRRHVDYITEKL 296
QY 258 Y-NAFLAGVPPVVLGSPRENYENIPADSFIVHEDYNSPSELAKYLVKEVDKNNKLYLYSF 316
DB 297 WRNAFLAGVPPVVLGSPRENYENIPADSFIVHEDYNSPSELAKYLVKEVDKNNKLYLYSF 356
QY 317 NWRKDFTNLPRFWESHACLDHVKRRH-QEYKSGVNLKWF 357
DB 357 RWRRSFAVHTSFWEQRCRTCAVOTSGDQPKSHNLADWF 398

RESULT 3
B36340
alpha(1,3)-fucosyltransferase (EC 2.4.1.6-) 4 precursor [validated] - human
N:Alternate names: CD15; ELAM-1 ligand fucosyltransferase (ELFT); FCT3A; FUC-TIV; myeloid
C:Species: Homo sapiens (man)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
R:Goelz, S.E.; Hession, C.; Goff, D.; Griffiths, B.; Tizard, R.; Newman, B.; Chi-Rosso,
Cell 63, 1349-1356, 1990
A:Title: ELFT: a gene that directs the expression of an ELAM-1 ligand.
A:Reference number: A36340; MUID:91084863
A:Accession: B36340
A:Molecule type: mRNA
A:Residues: 1-405 <GOE1>
A:Cross-references: GB:M58596; NID:g182068; PIDN:AAA63172.1; PID:g182069
A:Accession: A36340
A:Molecule type: mRNA
A:Residues: 'MRLWGAARKPSGAGWEKWEAEAPGAWSGRLPGKR','SGRKGRAVPGWASWPAHLAARPARHLGGAG
A:Cross-references: GB:M58597; NID:g182070; PIDN:AAA63173.1; PID:g182071
A:Note: the codon used as an initiator for this translation is not in a good context for
R:Low, J.B.; Kukowska-Latallo, J.F.; Nair, R.P.; Larsen, R.D.; Marks, R.M.; Macher, B.A
J. Biol. Chem. 266, 17467-17477, 1991
A:Title: Molecular cloning of a human fucosyltransferase gene that determines expression
A:Reference number: A40976; MUID:91373370
A:Accession: A40976
A:Status: Preliminary

A:Molecule type: DNA
A:Residues: 1-86, 'P', 88-405 <LOW>
A:Cross-references: GB:M65030; NID:g182791; PIDN:AAA92977.1; PID:g1236720
R:Kumar, R.; Potvin, B.; Muller, W.A.; Stanley, P.
J. Biol. Chem. 266, 21777-21783, 1991
A:Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but
A:Reference number: A41202; MUID:92042084
A:Accession: A41202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240, 'D', 242-400 <KUM>
A:Cross-references: GB:S65161; NID:g239005; PIDN:AAB20349.1; PID:g239006
C:Genetics: GDB:FUT4; CD15; FCT3A; FUC-TIV
A:Cross-references: GDB:L31563; OMIM:104230
A:Map position: 11q21-11q22
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
F:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-48/Domain: signal sequence #status predicted <SIG>
F:49-405/Product: alpha(1,3)-fucosyltransferase 4 #status predicted <MAT>
F:91,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 689.5; DB 2; Length 405;
Best Local Similarity 38.5%; Pred. No. 4.8e-45;
Matches 153; Conservative 60; Mismatches 109; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI---KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETTILV 68
DB 28 VCVLAAAGLTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWVPFGQTFDL-----TSCQAMFNTQGGHLLTDRSLYNKSHAVLIHHRDI-----SW---- 115
DB 69 WVEPFGGRDSAPRPPDCRLFRNISGCRLLTDRAAYGEAAQVLFHHRDLVKKVGPDPWPPW 128
QY 116 -----DLTNLPQO-----ARPPFOKVIWMNLESPHTP-OKSGIEHL 151
DB 129 GIOAHTAEVDLRVLDYEEAAAAAALATSPRPPGQRYWMNFSPSHSPLSLASNL 188
QY 152 FNLTATYRRSDIOVPYGLFTVSTNPFVFPVS-----KEKLVGVYVNNWNP 203
DB 189 FNWTLSEADSDVFPVGYLYPSHP--GDPSPGLAPPLSRKQGLVAVVSHWDERQAV 246
QY 204 KYNNELSKSIETIHYGQAF-GEVYNDKNLIPTISACKFYLSFENSISKDKYITEKL 261
DB 247 RYHQLSQHYTVDFVGGGQCPVFEIGLLHTVARYKFLAFENSQHLDYITEKLNRNAL 306
QY 262 LAGSPVVLGSPRENYENIPADSFIVHEDYNSPSELAKYLVKEVDKNNKLYLYSFENRMD 321
DB 307 LAGAVPVVLGSPRENYENIPADSFIVHEDYNSPSELAKYLVKEVDKNNKLYLYSFENRMD 366
QY 322 FTVNLPRFWESHACLDHVKRRH-QEYKSGVNLKWF 357
DB 367 YAVHTSFWEQRCRTCAVOTSGDQPKSHNLADWF 403

RESULT 4
A36669
galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) - human
N:Alternate names: alpha (1,3/1,4) fucosyltransferase; blood group Lewis alpha-4-fucc
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 29-Sep-1999
C:Accession: A36669; I39043; I39045; I39045; S12123
R:Kukowska-Latallo, J.F.; Larsen, R.D.; Nair, R.P.; Lowe, J.B.
Genes Dev 4, 1288-1303, 1990
A:Title: A cloned human cDNA determines expression of a mouse stage-specific embryoni
A:Reference number: A36669; MUID:91032981
A:Accession: A36669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-361 <KUK>
A:Cross-references: GB:X53578; NID:g28529; PIDN:CAA37641.1; PID:g28530
R:Cameron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122, 1995

J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal cells
A;Reference number: I39043; MUID:95378269
A;Accession: I39043
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-361 <RES>
A;Cross-references: EMBL:U27326; NID:g967188; PIDN:AAC50185.1; PID:g967189
A;Accession: I39044
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-361 <RE2>
A;Cross-references: EMBL:U27327; NID:g967190; PIDN:AAC50186.1; PID:g967191
A;Accession: I39045
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-361 <RE3>
A;Cross-references: EMBL:U27328; NID:g967192; PIDN:AAC50187.1; PID:g967193
C;Genetics:
A;Gene: GDB:FUT3; LE
A;Cross-references: GDB:135717; OMIM:111100
A;Map position: 19p13.3-19p13.3
A;Note: alternative splicing 5' to the coding region
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 33.9%; Score 667; DB 2; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.1e-43;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;

QY 66 ILVWVPFGTDLTSCQAMF-NIQCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
DB 65 ILLWTFPHFIPVALSRCSEMVPGTADCHITADRVKYPQADTVIVH---WDIMSNPKSR 120
QY 120 LPOQARPPFOKWIWMNLESTHTPQKSGIEHLNLTLYRRSDIQVPGFLTV-STNPF 178
DB 121 LPPSPRQGORWIFWNEPPLPNCQHLAEDRYENLTMSYRSDSDIETPYGWLPEWPSQPA 180
QY 179 --VFEPSPKELVCWVSNVNNPEHARVYKYNELSKSIEHTYQAGFGEYVNDKNLPTIS 236
DB 181 HPPLNLSAKTELVAWVSNWPKDSARVYQSLQAHKLVDPVYGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSFENSIHKDYITEKLY-NAFLAGSVVPVVLGSPSRNENYIPADSFHVEDYNSP 295
DB 240 RYKFYLAENSLHPDYITEKLRNLALEAWVPVVLGSPSRNERYERFLPPDAFIHVDQFSP 299
QY 296 SELAKYLKVDKNNKLYLSFNRKQFTVNLPR--FWESHACIACDHRKHQYKSVGNL 353
DB 300 KDLARVLQELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
DB 357 AAWF 360

RESULT 5
A42270
alpha(1,3) fucosyltransferase FUT5 - human
N;Alternate names: fucosyltransferase 5
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Sep-1999
A;Accession: A42270; I39046; I39047
R;Weston, B.W.; Nair, R.P.; Larsen, R.D.; Lowe, J.B.
J. Biol. Chem. 267, 4152-4160, 1992
A;Title: Isolation of a novel human alpha(1,3)fucosyltransferase gene and molecular cloning of the complementary DNA
A;Reference number: A42270; MUID:92156161
A;Accession: A42270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <RES>
A;Cross-references: GB:M81485; NID:g182490; PIDN:AAA98117.1; PID:g1280209
A;Note: sequence extracted from NCBI backbone (NCBIN:82825, NCBI:82826)
R;Cameron, H.S.; Szczepaniak, D.; Weston, B.W.

J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal cells
A;Reference number: I39043; MUID:95378269
A;Accession: I39046
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: EMBL:U27329; NID:g967194; PIDN:AAC50188.1; PID:g967195
A;Accession: I39047
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RE2>
A;Cross-references: EMBL:U27330; NID:g967196; PIDN:AAC50189.1; PID:g967197
C;Genetics:
A;Gene: GDB:FUT5
A;Cross-references: GDB:131644; OMIM:136835
A;Map position: 19p13.3-19p13.3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 33.9%; Score 667; DB 2; Length 374;
Best Local Similarity 43.7%; Pred. No. 2.2e-43;
Matches 131; Conservative 58; Mismatches 99; Indels 12; Gaps 8;

QY 66 ILVWVPFGTDLTSCQAMF-NIQCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQ 123
DB 78 ILLWTFPHFIPVALSRCSEMVPGTADCHITADRVKYPQADTVIVHWDIMVNSANLPPP 137
QY 124 ARPFPQKWIWMNLESTHTPQKSGIEHLNLTLYRRSDIQVPGFLTV-STNPF--VF 180
DB 138 TRPQGORWIFWNEPPLPNCQHLAEDRYENLTMSYRSDSDIETPYGWLPEWPSQPAHPL 197
QY 181 EVPSKELVCWVSNVNNPEHARVYKYNELSKSIEHTYQAGFGEYVNDKNLIFTISACKF 240
DB 198 NLSAKTELVAWVSNWPKDSARVYQSLQAHKLVDPVYGRSH-KPLPKGTMMETLSRYK 256
QY 241 YLSFENSIHKDYITEKLY-NAFLAGSVVPVVLGSPSRNENYIPADSFHVEDYNSPSELA 299
DB 257 YLAFENSLHPDYITEKLRNLALEAWVPVVLGSPSRNERYERFLPPDAFIHVDQFSPKDLA 316
QY 300 KYLKEVDKNNKLYLSFNRKQFTVNLPR--FWESHACIACDHRKHQYKSVGNLEKWF 357
DB 317 RYLQELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLOQESRYQTVRSTAAWF 373

RESULT 6
A45156
alpha(1,3)-fucosyltransferase FUT6 - human
N;Alternate names: alpha-(1,3)-fucosyltransferase Fuc-TVI; fucosyltransferase 6; Lewi
C;Species: Homo sapiens (man)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 29-Sep-1999
A;Accession: A45156; JCI228; I39050; I39051; I39052; I39053; I39054
R;Weston, B.W.; Smith, P.L.; Kelly, R.J.; Lowe, J.B.
J. Biol. Chem. 267, 24575-24584, 1992
A;Title: Molecular cloning of a fourth member of a human alpha(1,3)fucosyltransferase
A;Reference number: A45156; MUID:93077550
A;Accession: A45156
A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: GB:L01698; NID:g182792; PIDN:AAB03078.1; PID:g1280210
R;Koszdin, K.L.; Bowen, B.R.
Biochem. Biophys. Res. Commun. 187, 152-157, 1992
A;Title: The cloning and expression of a human alpha-1,3 fucosyltransferase capable of
A;Reference number: JCI228; MUID:92392318
A;Accession: JCI228
A;Molecule type: mRNA
A;Residues: 1-359 <KOS>
A;Cross-references: GB:M98825; NID:g182491; PIDN:AAA99222.1; PID:g182492
A;Note: the authors translated the codon GAC for residue 219 as Asn
R;Cameron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal cells
A;Reference number: I39043; MUID:95378269

Db 173 PWSQPAHPPLNLAKTELVAWNSGPNRSARVYQSLQAHKLVDVYGRSH-KPLPQG 231
Qy 230 NLIPITISACKYLYSFKSIHDKYITEKLY-NAFLAGSVVPLGSPSRENYENIIPADSIH 288
Db 232 TMMETLSRYKFLAFENSLHPDYITEKLWRNLALEAWAVPVVLGSPSRNRYERFLPDPAFIH 291
Qy 289 VEDYNSPSELAKYLYKEVDKNNKLYLSPFNWRKDTVNLPR--FWESHACIAC 338
Db 292 VDFQSPDLARYLQELDKOHARYLSYFRWRETLR---PRSFWSALAFCKAC 340

RESULT 9
A54057
alpha(1,3)-fucosyltransferase (EC 2.4.1.1) 7 precursor - human
N;Alternate names: leukocyte fucosyltransferase FucTVII
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 20-Apr-2000
C;Accession: A54057; MUID:94237894
R;Sasaki, K.; Kurata, K.; Funayama, K.; Nagata, M.; Watanabe, E.; Ohta, S.; Hanai, N.; J. Biol. Chem. 269, 14730-14737, 1994
A;Title: Expression cloning of a novel alpha(1,3)-fucosyltransferase that is involved in b
A;Reference number: A54057; MUID:94237894
A;Accession: A54057
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-342 <SAS>
A;Cross-references: GB:X78031; NID:g516292; PIDN:CAA54962.1; PID:g516293
R;Natsuka, S.; Gersten, K.M.; Zenita, K.; Kannagi, R.; Lowe, J.B. J. Biol. Chem. 269, 16789-16794, 1994
A;Title: Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyl
A;Reference number: A53713; MUID:94266898
A;Accession: A53713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-160, 'A', 163-303, 'SV', 306-342 <NAT>
A;Cross-references: GB:U08112; NID:g520463; PIDN:AAA56869.1; PID:g520464
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:373982
A;Map position: 9pter-9qter
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-34/Domain: signal sequence #status predicted <Sig>
F;35-342/Product: alpha(1,3)-fucosyltransferase 7 #status predicted <MAT>
F;81,291/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.4%; Score 619; DB 2; Length 342;
Best Local Similarity 43.0%; Pred. No. 9.1e-40;
Matches 129; Conservative 49; Mismatches 108; Indels 14; Gaps 8;

Qy 65 TILVWVWPF-GQTFDLTS--CQAMFNIQGCCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
Db 48 TILVWHPFTDPPPELSDTC-TRYGIARCHLSANRSLASADAVVHHRLQTRRSLP 106
Qy 122 QOARPPQKWTWMLNLESPTHTPQSGIEHLNLTITRDSDIQVPYGLFVSNPFFVE 181
Db 107 LAQPRGQPMWASMESPTHTGSLKGIENWVLSYRDSRSDIFVYGRLEPHMGSP-P 165
Qy 182 VPSKEKLCVWVSNWNPHEHARVKNYELSKSIEHTYQGAEGYVNDKNLPTISACKFY 241
Db 166 LPAKSRVAWVSNFQERQLRARLYQLAPHLRVDFVGRNGRPLCASCCLPTVAQYRFY 225
Qy 242 LSFENSHDKYITEKLY-NAFLAGSVVPLGSPSRENYENIIPADSIHVEDYNSPSELAK 300
Db 236 LSFENSHQRDYITEKFWRNALVAGTPVVLGPPRATYEAFPADAFVHVDGFSARELAA 285
Qy 301 YLKEVDKNNKLYLSPFNWRKDTVNLPRFWESHACIACD---HVKRHOEYKSVGNLEKWF 357
Db 286 FL--TGMNESYQRFARWRDLRVLEFDWREFAICDRIYPLPRSOVYE---DLEGWF 340

RESULT 10

I39049
alpha(1,3)-fucosyltransferase FUT6-related splice form II - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 29-Sep-1999
C;Accession: I39049
R;Cameron, H.S.; Szczepaniak, D.; Weston, B.W. J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in m
A;Reference number: I39043; MUID:95378269
A;Accession: I39049
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-304 <RES>
A;Cross-references: EMBL:U27332; NID:g967200; PIDN:AAC50191.1; PID:g967201
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:135180; OMIM:136836
A;Map position: 19p13.3-19p13.3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: alternative splicing

Query Match 24.3%; Score 478.5; DB 2; Length 304;
Best Local Similarity 43.0%; Pred. No. 4.1e-29;
Matches 98; Conservative 42; Mismatches 81; Indels 7; Gaps 6;

Qy 55 STKTDYFNETTILVWVWPFQTFDLTSCQAMP-NIQGCHLTDRSLYNKSHAVLIHHRDI 113
Db 53 STGTPAHSLIPLILLWTWPFNKPIALPRGSEMVPGTADCNITADRRKVPQADAVIVHREV 112
Qy 114 SWD-LTNLPQOARPPQKWIWNNLESPTHTPQSGIEHLNLTITRDSDIQVPYGLFT 172
Db 113 MYNPAQLPRSPRQGRQWIFSMESHCWOLKAMDGYFNLTWYSRSDSIFTYGVWLE 172
Qy 173 V-STNPF--VEEVPSEKLCVWVSNWNPHEHARVKNYELSKSIEHTYQGAEGYVNDK 229
Db 173 PWSQPAHPPLNLAKTELVAWNSGPNRSARVYQSLQAHKLVDVYGRSH-KPLPQG 231
Qy 230 NLIPITISACKYLYSFKSIHDKYITEKLY-NAFLAGSVVPLGSPSRENYENIIPADSIH 276
Db 232 TMMETLSRYKFLAFENSLHPDYITEKLWRNLALEAWAVPVVLGSPSRN 279

RESULT 11
TI5270
hypothetical protein F59E12.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: TI5270
R;Johnson, D. submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E12.
A;Reference number: Z18318
A;Accession: TI5270
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-414 <JOH>
A;Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088845; PIDN:AAB54261.1; GSPD3
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
A;Gene: CESP:F59E12.13
A;Map position: 2
A;Introns: 90/3; 237/2; 279/3; 309/2; 339/2; 388/3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 15.8%; Score 311; DB 2; Length 414;
Best Local Similarity 28.0%; Pred. No. 3.8e-16;
Matches 98; Conservative 58; Mismatches 120; Indels 74; Gaps 17;

Qy 66 ILVWVWPFQTFD---LTSCQAMFNIQGCCHLTDRSLYNKSHAVLIHHRDISWDLTNLP- 121
Db 67 ILYWTITFGATVPSTALSDCPGL--TDRCVITDRHQLDADAVVFFHAADIS----KEPL 120
Qy 122 QOARPPQKWTWMLNLESPTHTPQSG-----IEHLNLTITLYRRSD 163

Db 121 PVSRRKPDQIFVNSME---TPDSGRFAVPGKINVLNKKPIYLDGFENWTSTHLYSD 176
QY 164 IQPVYGFGLVST---NPFVFEVPS-----KEKLYCVVSVNWNPEHARVKYNNELS 210
Db 177 AIHKYGTFLIPTLAESRGFKVQSYVQPKRLVKYMKGFGLISNCHYKSKRELALQELG 236
QY 211 KSTIEHTYQAGEVND---KNLPTISAC-----KFYLSFENSIIHKDYITEKLYNA 260
Db 237 KHLNV-TIG---GKASDRLKSCIPAGVECDIVFEQYFYIAIENTVCNDIVTEKWSR 292
QY 261 FLAGSVPVVLGSPRENYENYIPADSFIVHEDYNSPSELAKYLKEVDKNNKLYSYFNWR- 319
Db 293 ITVPSIPVW---RRRYQNILPKPSFIAMDYKNPSEMANHLRSEANSTAYGEYFWRQ 350
QY 320 KQTVNLPRFWSHA-----CLACDHVKRQE-----YKSGVGNLEKWFVN 359
Db 351 KGLWTSAP--WNAAGYRNGLCRVCELLKAKDNETEVKSYDNIWKFND 398
RESULT 12
T16799
hypothetical protein T05A7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16799
R:Chissoe, S.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid T05A7.
A:Reference number: 218580
A:Accession: T16799
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1652 <CHI>
A:Cross-references: EMBL:U40028; NID:g1055143; PID:g1055144; PIDN:AAA81114.1; CESP:T05A7
C:Genetics:
A:Gene: CESP:T05A7.5
A:Introns: 7/1; 43/3; 71/3; 132/1; 203/2; 247/3; 290/2; 315/3; 351/3; 407/2; 449/1; 504/
4/1; 1535/3; 1565/2; 1609/3
Query Match 15.6%; Score 308; DB 2; Length 1652;
Best Local Similarity 31.3%; Pred. No. 4.3e-15;
Matches 82; Conservative 53; Mismatches 103; Indels 24; Gaps 11;
QY 79 LFSQAMFNIOGCHLTDRSLYNKSHAVLIHHRDI--SWDNLNLPQQAARPPQKWIWNL 136
Db 1396 LATCPDVQNY--CRITQEESEFDNADAVLFHNADYRGSTDKFKMKSORKPGVPYVLWSL 1453
QY 137 ESPTHTPOKSGIEHLNLTLYRRSDIQVPYGFVLTSTNPFVFEV---PSKEKLVGV 192
Db 1454 ESPTNDMFRPD-SHMINWTMTYRTDSVWAPYGTIVKLNPPVEVDLNAIWEGTKTATWL 1512
QY 193 VSNWNPHEARVKYNE-LSKSTIEHTYQAGEYV-----NDKN--LIPTISACKFYL 242
Db 1513 ASNCITQNHFRDLIKKIIDNGFEIDWGNCG-KQVSCAGVDNQSPCVLELIKPYKEVI 1571
QY 243 SPENSIIHKDYITEKLYNAFL-AGSVPVVLGSPRENYENY-IPADSFIVHEDYNSPSELAK 300
Db 1572 SMENSCNDYVTEKFWKALNDRMTIPVL--ARKYKDLGVDPDSAYIAVDYATLDFELA 1629
QY 301 YLKEYDKNNKLYSYFNWRKDF 322
Db 1630 HVKYNKEKDLFLSYHQWKEW 1651
RESULT 13
T23491
hypothetical protein K08F8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23491
R:Smyle, R.
submitted to the EMBL Data Library, October 1995

A:Reference number: 219747
A:Accession: T23491
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <SWIL>
A:Cross-references: EMBL:Z66497; PIDN:CAA91285.1; GSPDB:GN00020; CESP:K08F8.3
A:Experimental source: clone K08F8
C:Genetics:
A:Gene: CESP:K08F8.3
A:Map position: 2
A:Introns: 30/2; 53/3; 133/1; 195/3; 242/3; 277/3; 307/2; 342/3; 382/2
Query Match 14.3%; Score 281.5; DB 2; Length 451;
Best Local Similarity 30.1%; Pred. No. 7.7e-14;
Matches 86; Conservative 44; Mismatches 99; Indels 57; Gaps 12;
QY 67 LVWVPFGQTDLTSCQAMFNIOG-----CHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
Db 137 LILSNAGHSQD-----NLQCGPDWNCETQVRARAPDADAVLIAHMDNDF----VP 184
QY 122 QQAARPPQKWIWNLNLSPTHTPOKSGIE-----HLNLTLYRRSDIQVPYGFV----- 171
Db 185 K-----PNQYVVVFSQESPA-----SGIQIPRPDIYINMTLGRHDTPAGSPYGVTKLGAK 236
QY 172 -----TVSTNPFVFEVPSKEKLVGVSVNWNPEHARVKYNNELSKSTIEHTYQ----- 220
Db 237 SRKTGOVVDAN-----LVNGKAKGAWFVSHCOTNSKREDFVKKLOKHLQIDYIGCGGPMK 292
QY 221 -AFGEVVDNKNLIPITISACKSYLSFENSIIHKDYITEKLYNAFLAGS--VPVVLGSPRENYE 278
Db 293 CARGDSKCDTML---DIDYHFVTFPENSICEDIVTEKLVKSGYQNTIIPVL--ARKLVE 347
QY 279 NYIPADSFIVHEDYNSPSELAKYLKEVDKNNKLYSYFNWRKDFTV 324
Db 348 FVPPNSFIADDDFKSVKEMGDYLNLMNNKTAYMEYFEWRHDKV 393
RESULT 14
H96742
hypothetical protein F17M19.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96742
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alor
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, A.R.; Creasy, T.H.; Dewar,
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talic
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <STO>
A:Cross-references: GB:AE005173; NID:g6978923; PIDN:AAF34315.1; GSPDB:GN00141
C:Genetics:
A:Gene: F17M19.14
A:Map position: 1
Query Match 11.4%; Score 224.5; DB 2; Length 393;
Best Local Similarity 26.2%; Pred. No. 1.4e-09;
Matches 90; Conservative 47; Mismatches 129; Indels 77; Gaps 14;
QY 39 SPMSASSVLMKNFFSTKTIDYFNETTILV--VWVPFGQTDLTSCQAMFNIOGCHLTLD 96
Db 82 SLQFEGCGCKLKKH-----VKVLVKGWTWIPDNLENLYSCR-----CGMT-- 121
QY 97 RSLYNKSHAVLIHHRDISWDLTNLPQQAARPPQKWIWNLNLSPTHTPOKSGIEHLNLT 156
A:Reference number: 219747
A:Accession: T23491
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <SWIL>
A:Cross-references: EMBL:Z66497; PIDN:CAA91285.1; GSPDB:GN00020; CESP:K08F8.3
A:Experimental source: clone K08F8
C:Genetics:
A:Gene: CESP:K08F8.3
A:Map position: 2
A:Introns: 30/2; 53/3; 133/1; 195/3; 242/3; 277/3; 307/2; 342/3; 382/2

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Db 122 -CLWTKSSVLADSPDALLFETTPPLQRRVGDPLRVYMELEAGR---KRSREDIF---I 174
QY 157 TYRDSIQVYGYGLTVSTNPFVFEVPSK--EKLVCWVSVNWNPEHARVYKYNELSKS-- 212
Db 175 SYHAKDDVQTYAGSLFHNRRNHYHSPHKNDVLVYSSSRCLPHRDR-----LAKSL 228
QY 213 --JEIHTYGA-----FGEYNDKN-----LIPTISACKFYLSFENSIH 249
Db 229 DLPHHSFGKLNNGVGLDSALSMPYECVAEHAENAKWYDHLHCAMSHYKFLAIENTAV 288
QY 250 KDYTEKLYNAFLAGSVVYVLPGRSRENYENIPADSFHVEDYNSPSELAKYLKEVDKNN 309
Db 289 ESYVTEKLFALDGSVPYIFGAS--NVQFVPPHSHVSDGSKFGSMQELAAAYVKRLGDDP 346
QY 310 KLYLSYFNWR-----KDFVTNLPFRWESHACLADHVKR 343
Db 347 VAYSEYHAWRRCLGMNGYKTRAVSL-----DTLPCLCEISR 385

RESULT 15
F96533
probable fucosyltransferase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96533
R:Rheologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F96533
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: GB:AE005173; NID:g10120428; PIDN:AAG13053.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14J22.8
A:Map position: 1

Query Match 10.3%; Score 203.5; DB 2; Length 513;
Best Local Similarity 25.7%; Pred. No. 8.3e-08;
Matches 77; Conservative 50; Mismatches 122; Indels 51; Gaps 15;

QY 56 TKTDYFNETHILVWVWPFQGFDTLSCQ---AMFNIOGCH---LTDRSLYNKSHA---V 106
Db 70 TLTDFTQSPSL-----SQSPFARSRRKKIGLFTDRSCEWLMREDSVTSYRDFTKDPI 123
QY 107 LIH--HRDISW---DLT-----NLPQA---RPPQKWIWNLESPTHTPOKSGIEHL 151
Db 124 FISGGERDFQWCSVDCTFGSSCKTPDAAGLGQKPGTSLIIRSWESAQYPEN----- 177
QY 152 FNLTLYRRSDI-----QVPYGLTVSTNPFVFEV--PSKEKLYCWV--VSNWNPEHA 201
Db 178 -DLAQARRRGYDVMVTTSLSSDPVGVFSNAEYDIMSVPQKTERATAAAAFISNCGARNE 236
QY 202 RVXYYNELSK-STEIHTYGAQGEYVNDKNLIPTISACKFYLSFENSIHKDYITEKLYNA 260
Db 237 RLQALEALMTNKIDSYGCKHRNRDGVKVEALKRYKFSLAFENTNEEDYVTEKFFQS 296
QY 261 FLAGSVVWVLGRSRENYENIPA--DSFIHVEDYNSPSELAKYLKEVDKNNKLYSYFNWR 319
Db 297 LVAGSVVYVYVGP--PNIEEFAPASDSFLHKITMEDVEPVAKRMKYLAAANPAAYNQTLRWK 354
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Search completed: October 8, 2002, 16:54:37
Job time : 17.5 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:06:57 ; Search time 8.5 Seconds
(without alignments)
(1635.332 Million cell updates/sec)

Title: US-09-744-748-2

Perfect score: 1970

Sequence: 1 WTSTSGILRPPLIVCIILG.....HVKRHQEKSVGNLEKFWFN 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	703	35.7	433	1 FUT4_MOUSE	Q1127 mus musculus
2	690.5	35.1	433	1 FUT4_RAT	Q6294 rattus norv
3	687.5	34.9	405	1 FUT4_HUMAN	P22083 homo sapien
4	667	33.9	361	1 FUT3_HUMAN	P21217 homo sapien
5	667	33.9	374	1 FUT5_HUMAN	Q11128 homo sapien
6	666	33.8	374	1 FUT5_PANTR	P56433 pan troglod
7	665	33.8	365	1 FUT3_BOVIN	Q11126 bos taurus
8	662.5	33.6	359	1 FUT6_HUMAN	P51993 homo sapien
9	660	33.5	372	1 FUT3_PANTR	O19058 pan troglod
10	659.5	33.5	359	1 FUT6_PANTR	P56434 pan troglod
11	619	31.4	342	1 FUT7_HUMAN	Q11130 homo sapien
12	579	29.4	389	1 FUT7_MOUSE	Q11131 mus musculus
13	353	17.9	503	1 FUT7_DROME	Q9VUL9 drosophila
14	295.5	15.0	425	1 FUTC_DROME	P83088 drosophila
15	254.5	12.9	443	1 FUTB_DROME	Q9VLC1 drosophila
16	224.5	11.4	401	1 FU13_ARATH	Q9C8W3 arabidopsis
17	203.5	10.3	513	1 FU12_ARATH	Q9FX97 arabidopsis
18	201	10.2	501	1 FU11_ARATH	Q91JK1 arabidopsis
19	106	5.4	663	1 GRIA_BACCE	O85467 bacillus ce
20	105	5.3	537	1 UGT5_CAEEL	Q20086 caenorhabdi
21	99	5.0	810	1 233A_HUMAN	O06730 homo sapien
22	98.5	5.0	623	1 RPOC_GUITH	O78484 guillardia
23	98.5	5.0	781	1 HELI_HSVSA	Q01014 herpesvirus
24	97.5	4.9	638	1 Y153_HUMAN	Q14166 homo sapien
25	96	4.9	387	1 CXY_CLOSR	P40942 clostridium
26	96	4.9	566	1 GUNB_PAELA	P23550 paenibacill
27	96	4.9	2059	1 TEGU_HSV7J	P23362 human herpe
28	95	4.8	1480	1 CFTR_HUMAN	P13569 homo sapien
29	93.5	4.7	1147	1 NRDC_HUMAN	O43847 homo sapien
30	92	4.7	1092	1 DHE2_YEAST	P33327 saccharomyc
31	91.5	4.6	1173	1 NIFU_ENTAG	P19543 enterobacte
32	91	4.6	482	1 YQ53_BACAN	Q9RMX9 bacillus an
33	91	4.6	772	1 LP1G_DROME	P11997 drosophila

34	91	4.6	1026	1 EX5B_CHLMU	Q9PLT8 chlamydia m
35	90.5	4.6	584	1 MUTL_BUCAI	P57633 buchera ap
36	90.5	4.6	986	1 EPIB_STAEP	P30193 staphylococ
37	90	4.6	438	1 RGSB_MOUSE	Q9Z2H1 mus musculu
38	90	4.6	471	1 CD36_BOVIN	P26201 bos taurus
39	89.5	4.5	461	1 MYH_SCHPO	Q10159 schizosacch
40	89.5	4.5	516	1 DHCR_HUMAN	Q15392 homo sapien
41	89.5	4.5	602	1 PRIM_MYCPU	Q98B33 mycoplasma
42	89.5	4.5	934	1 SYLI_SULSO	P58176 sulfolobus
43	89	4.5	678	1 GSH1_YEAST	P32477 saccharomyc
44	89	4.5	1364	1 BLM_XENLA	Q9DEV9 xenopus lae
45	89	4.5	1581	1 ARO1_PNECA	Q12659 p pentafunc

ALIGNMENTS

RESULT 1

ID	FUT4_MOUSE	STANDARD	PRT	433 AA.
AC	Q11127;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 4) (FUCT-IV).			
GN	FUT4 OR ELFT.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96027607; PubMed=7559635;			
RA	Gersten K.M., Natsuka S., Trinchera M., Petryniak B., Kelly R.J.,			
RA	Hiraiwa N., Jenkins N.A., Gilbert D.J., Copeland N.G., Lowe J.B.;			
RT	"Molecular cloning, expression, chromosomal assignment, and tissue-specific expression of a murine alpha-(1,3)-fucosyltransferase locus corresponding to the human ELAM-1 ligand fucosyl transferase.";			
RT	J. Biol. Chem. 270:25047-25056(1995).			
RL	[2]			
RN	SEQUENCE FROM N.A. (SHORT FORM).			
RP	STRAIN=129/SV; TISSUE=Liver;			
RC	MEDLINE=97037075; PubMed=8862722;			
RX	Ozawa M., Muramatsu T.;			
RA	"Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene that shows homology with the human alpha-1,3 fucosyltransferase IV gene.";			
RT	J. Biochem. 119:302-308(1996).			
RL	- - FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.			
CC	- - PATHWAY: GLYCOSYLATION.			
CC	- - SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.			
CC	- - ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	- - TISSUE SPECIFICITY: HIGHEST EXPRESSION IN STOMACH AND COLON. IT ALSO EXPRESSED IN THE LUNG, TESTIS, UTERUS, SMALL INTESTINE AND TO A LESSER EXTENT IN SPLEEN, AND OVARY. PRESENT IN TRACE AMOUNTS IN BRAIN, THYMUS, HEART, SMOOTH MUSCLE, KIDNEY AND BONE MARROW. NOT FOUND IN LIVER, SALIVARY GLAND AND PANCREAS.			
CC	- - SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.			

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DR EMBL: U33457; AAC52269.1; -
DR EMBL: D63380; BAA09697.1; -

DE fucosyltransferase).
GN FUT4 OR ELFT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RC TISSUE=Peripheral blood leukocytes;
RX MEDLINE=91373370; PubMed=1716630;
RA Lowe J.B., Kukowska-Latallo J.F., Nair R.P., Larsen R.D., Marks R.M.,
RA Macher B.A., Kelly R.J., Ernst L.K.;
RT "Molecular cloning of a human fucosyltransferase gene that determines
RT expression of the Lewis x and VIM-2 epitopes but not ELAM-1-dependent
RT cell adhesion.";
RL J. Biol. Chem. 266:17467-17477(1991).
RN [2]
RN
RX
RP
RC
RX MEDLINE=91084863; PubMed=1702034;
RA Goelz S.E., Hession C., Goff D., Griffiths B., Tizard R., Newman B.,
RA Chi-Rosso G., Lobb R.;
RT "ELFT: a gene that directs the expression of an ELAM-1 ligand.";
RL Cell 63:1349-1356(1990).
RN [3]
RN
RX
RP
RC
RX MEDLINE=92042084; PubMed=1718983;
RA Kumar R., Potvin B., Muller W.A., Stanley P.;
RT "Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes
RT ELFT but does not confer ELAM-1 recognition on Chinese hamster ovary
RT cell transfectants.";
RL J. Biol. Chem. 266:21777-21783(1991).
CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
CC
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CC or send an email to license@isb-sib.ch).
DR EMBL; M65030; AAA92977.1; -;
DR EMBL; M58596; AAA63172.1; -;
DR EMBL; M58597; AAA63173.1; ALT_INIT.
DR EMBL; S65161; AAB20349.1; -;
DR PIR; A36340; A36340.
DR MIM; 104230; -;
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 48 405 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 87 87 P -> R (IN REF. 2 AND 3).
FT CONFLICT 241 241 E -> D (IN REF. 3).
SQ SEQUENCE 405 AA; 45569 MW; DE72E1FDC390268D CRC64;
Query Match 34.9%; Score 687.5; DB 1; Length 405;
Best Local Similarity 38.5%; Pred. No. 2.5e-44;
Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;
QY 15 VCIILGCFMAC--LLIYI----RPTNSWIFSPMESASSVLKMKNFSTKTDYFNFTILV 68
DB 28 VCVLAAAGLICTALITVACGQLPLPWA-SPTPS-----RPVGVLL 68

QY 69 WVPFGQTFDL-----TSCQAMFNIGQCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115
DB 69 WVEPFGGRDSAPRPPDPDCPLRFNIGSRLLTDRASYGEAQAVLFHHRDLVKGPPDPWPPPW 128
QY 116 -----DLTNLPQO-----ARPPFOKWIMNLESPTHTP-OKSGIEHL 151
DB 129 GQAHTAEVDLRVLDYEEAAAAAALATSSPPRPGORVWMNMFSPSHSGPLKSLASNL 188
QY 152 FNLTLYRRDSDIQVPYGFLLTVSTNPFVFPVS-----KEKLVQWVYNNWNPHEHARV 203
DB 189 FNNLTSLYRADSDFVPVGYLYPRSHP--GDPPSLAPLSRKQGLVAVVYSHWDERQARV 246
QY 204 KYNEILSKSTEIHTYQOAF--GEVYNDKNLPTISACKFYLSFSPENSIHKDIITEKLY-NAF 261
DB 247 RYTHQLSQHVTVDVFGRGPGQVPPEIGLLHTVARYKFLAFENSQHLDIITEKLWRNAL 306
QY 262 LAGSVPVVLGLSPRENYENIPADSFHVEDYNPSSELAKEYLKEVDKNKLYLSVFNWRKD 321
DB 307 LAGAVPVVLGLDPRANYERFVPRGAFIHVDFFPSSASSLASYLFLDRNPAVIRRYFFHWRSS 366
QY 322 FTVNLPFWESHACLACDHVKRHOEY--KSYGNLEKWF 357
DB 367 YAVHITSEWDEPWCRCVQAVORAGDRPKSIRNLASWF 403
RESULT 4
ID FUT3_HUMAN STANDARD; PRT; 361 AA.
AC P21217; Q99448; Q99449;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis
DE alpha-4-fucosyltransferase) (Lewis Fx) (Fucosyltransferase 3) (FUCT-
DE III)
GN FUT3 OR LE OR FT3B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91032981; PubMed=1977660;
RA Kukowska-Latallo J.F., Larsen R.D., Nair R.P., Lowe J.B.;
RT "A cloned human cDNA determines expression of a mouse stage-specific
RT embryonic antigen and the Lewis blood group
RT alpha(1,3/1,4)fucosyltransferase.";
RL Genes Dev. 4:1288-1303(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95378269; PubMed=7650030;
RA Cameron H.S., Szczepaniak D., Weston W.;
RT "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
RT genes in normal tissues. Alternative splicing, polyadenylation, and
RT isoforms.";
RL J. Biol. Chem. 270:20112-20122(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Squamous cell carcinoma;
RA Rahim I., Schmidt L.R., Wahl D., Drayson E., Maslanik W.,
RA Stranahan P.L., Pettijohn D.E.;
RT "Isolation and expression of human alpha (1,3/1,4)
RT fucosyltransferase.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP VARIANT LE(-) MET-105.
RX MEDLINE=94059067; PubMed=8240322;
RA Elmgren A., Rydberg L., Larson G.;
RT "Genotypic heterogeneity among Lewis negative individuals.";
RL Biochem. Biophys. Res. Commun. 196:515-520(1993).
RN [5]

QY 296 SELAKYLKEVDKNNKLYLSEYFNKRKDFVNLPR--FWESHACIACDHHVKKHQEYKSVGNL 353
 Db 300 KDLARYLQELDKHARYLSYFRWRETLR---PRFSWALDFCKACKWKLQESRYQTVRSI 356
 QY 354 EKWF 357
 Db 357 AAWF 360

RESULT 5
 FUT5_HUMAN STANDARD; PRT; 374 AA.
 AC Q11128;
 DT Q1-OCT-1996 (Rel. 34, Created)
 DT Q1-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 5) (FUCT-V).
 GN FUT5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood leukocytes;
 RX MEDLINE=92156161; PubMed=7650030;
 RA Weston B.W., Nair R.P., Larsen R.D., Lowe J.B.;
 RT "Isolation of a novel human alpha (1,3)fucosyltransferase gene and molecular comparison to the human Lewis blood group alpha (1,3/1,4)fucosyltransferase gene. Syntenic, homologous, nonallelic RT genes encoding enzymes with distinct acceptor substrate specificities.";
 RT J. Biol. Chem. 267:4152-4160(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon, Kidney, and Liver;
 RX MEDLINE=95378269; PubMed=7650030;
 RA Cameron H.S., Szczepaniak D., Weston B.W.;
 RT "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal tissues. Alternative splicing, polyadenylation, and isoforms.";
 RT J. Biol. Chem. 270:20112-20122(1995).
 RL CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS X/SSEA-1 AND SIALYL LEWIS X ANTIGENS.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-(ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- TISSUE SPECIFICITY: LIVER, COLON AND TESTIS AND TRACE AMOUNTS IN T-CELLS AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
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 CC -----
 DR EMBL; M81485; AAA98117.1; -;
 DR EMBL; U27329; AAC50188.1; -;
 DR EMBL; U27330; AAC50189.1; -;
 DR MIM; 136835; -;
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.

FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 35 374 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 374 AA; 43008 MW; B825281521B57939 CRC64;

Query Match 33.9%; Score 667; DB 1; Length 374;
 Best Local Similarity 43.7%; Pred. No. 7.7e-43;
 Matches 131; Conservative 58; Mismatches 99; Indels 12; Gaps 8;
 QY 66 ILVVMVPGQTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISMD-LTNLPQQ 123
 Db 78 ILLWTVPFNTPVALPRCSEMVPGAACDNITADSSVYQADAVIVHHWDIMYNSANLPPP 137
 QY 124 ARPPFQKWIWNLESPTHTPKSGIEHLENLTLTYRSDIOVPYGFELTV-SINPF--VF 180
 Db 138 TRPGOGKWIWFSESPSNCRHLEALDGYFNLTWSYSDSDIFTYPGWLEPWSQPAHPPL 197
 QY 181 EVPSKEKLCVWVSNWNPENHARVYKYNELSKSIEHTHYGOAFGEYVNDKKNLIPTISACKF 240
 Db 198 NLSAKTELVAWAVSNWKPDSARYYQSLQAHKLDVYVGRSH-KPLPKGTMTETLSRYKF 256
 QY 241 YLSFENSIHKDYITEKLY-NAFLAGSVVVLGSPSRENYENIIPADSFHVEDYNSPSELA 299
 Db 257 YLAFENSLHPDYITEKLRNLEAWAVVVLGSPSRYERFLPDPAFIVDDFQSPKDLA 316
 QY 300 KYLKEVDKNNKLYLSEYFNKRKDFVNLPR--FWESHACIACDHHVKKHQEYKSVGNLEKWF 357
 Db 317 RYLQELDKHARYLSYFRWRETLR---PRFSWALAECKACKWKLQESRYQTVRSI 373

RESULT 6

FUT5_PANTR STANDARD; PRT; 374 AA.
 AC P56433;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (fucosyltransferase 5) (FUCT-V).
 GN FUT5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98037800; PubMed=9368041;
 RA Costache M., Apoil P.-A., Cailliau A., Elmgren A., Larson G., Henry S., Blancher A., Iordachescu D., Oriol R., Mollicone R.;
 RT "Evolution of fucosyltransferase genes in vertebrates.";
 RL J. Biol. Chem. 272:29721-29728(1997).
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS X/SSEA-1 AND SIALYL LEWIS X ANTIGENS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-(ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
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 CC -----
 DR EMBL; M81485; AAA98117.1; -;
 DR EMBL; U27329; AAC50188.1; -;
 DR EMBL; U27330; AAC50189.1; -;
 DR MIM; 136835; -;
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.

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CC -----
CC EMBL: Y14034; CAA74361.1;
CC InterPro: IPR001503; Glyco_transf_10.
CC Pfam: PF00852; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Signal-anchor; Golgi stack.
CC DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT
CC FT DOMAIN 35 374 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 374 AA; 43034 MW; 3F35DEE8A8F1A2E2 CRC64;
CC -----
CC Query Match 33.8%; Score 666; DB 1; Length 374;
CC Best Local Similarity 43.0%; Pred. No. 9,2e-43;
CC Matches 129; Conservative 59; Mismatches 100; Indels 12; Gaps 7;
CC -----
CC QY 66 ILVWVWPFQGTDLTSCQAMF-NIOGCHLTDRSLYKNSHAVLIHHRDISWD-LTNLPQQ 123
CC DB 78 ILLWTWPFNPVALPCSEKVPKADCNITADSNVYQADAVIVHWDIMNPSANLPPP 137
CC QY 124 APPPKQKWMNLESPHTTPQKSGIEHNLTLTYRSDIOVPGFLTVSTNPV---F 180
CC DB 138 TPQGGRIWFSWESFNSCRHLEADGFLNLTMSRSDSDIFTTPYGLQPSGGQVHPPL 197
CC QY 181 EYPSKEKLVGVVSNWNPENHARVYKYNLSKSIETHYCOAPGEYVNDKNLPTISACKF 240
CC DB 198 NLSAKTELAVANWNGNSAKRVYQSLOAHLKVDVYGRSH-KPLPGTMMETLSRYKF 256
CC QY 241 YLSFENSIHKDYITEKLY-NAFLAGSVVPVGLPSRENYENIPADSFIVHEDYNSPSELA 299
CC DB 257 YLAFENSLHPDYITEKLRNLEAWAVPVVGLPSRSNTERFLPPDAFTHVDDFQSPKDLA 316
CC QY 300 KYLKEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLDHVRHQRKYSVGNLEKWF 357
CC DB 317 RYLQELDKDHARYLSYFRWRETLR---PRSFSWALDFKACKWKLOQRYQTVRSIAAWF 373
CC -----
CC RESULT 7
CC ID FUT3_BOVIN STANDARD; PRT; 365 AA.
CC AC Q11126;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 01-MAR-2002 (Rel. 41, Last annotation update)
CC DE Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis
CC DE alpha-4-fucosyltransferase) (Lewis Ff) (Fucosyltransferase 3) (FUCT-
CC DE IL) (FUTB).
CC OS Bos taurus (Bovine).
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC CC Bovidae; Bovinae; Bos.
CC OX NCBI_TaxID=9913;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA MEDLINE-97236840; PubMed-9079712;
CC RA Oulmouden A., Wierinckx A., Petit J.-M., Costache M., Palcic M.M.,
CC RA Mollicone R., Oriol R., Julien R.;
CC RT "Molecular cloning and expression of a bovine alpha(1,3)-
CC RT fucosyltransferase gene homologous to a putative ancestor gene of the
CC RT human FUT3-FUT5-FUT6 cluster."
CC RL J. Biol. Chem. 272:8764-8773(1997).
CC RL -!- FUNCTION: MAY CATALYSE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
CC INVOLVED IN THE EXPRESSION OF SIALYL LEWIS X AND LEWIS X/SEA-1
CC ANTIGENS. IT MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION.
CC CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
CC CC N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
CC CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
CC -----
CC -!- PATHWAY: GLYCOSYLATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -!- TISSUE SPECIFICITY: LIVER, KIDNEY, LUNG AND BRAIN.
CC -!- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL
CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X87810; CAA61079.1;
CC InterPro: IPR001503; Glyco_transf_10.
CC Pfam: PF00852; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Signal-anchor; Golgi stack.
CC DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT
CC FT DOMAIN 35 365 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (PROBABLE).
CC FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (PROBABLE).
CC FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (PROBABLE).
CC SEQUENCE 365 AA; 42654 MW; 18715A361B0025D3 CRC64;
CC -----
CC Query Match 33.8%; Score 665; DB 1; Length 365;
CC Best Local Similarity 38.9%; Pred. No. 1.1e-42;
CC Matches 143; Conservative 68; Mismatches 115; Indels 42; Gaps 12;
CC -----
CC QY 11 PFLIVCIILG-CFMACLLI---YIKPTNSWI-----FSPMESASSVLKMKNFSTKTDY 60
CC DB 18 PGLLIQLLALCFTSYLRMSQEKPKPDMWSELGAPSOATEGSSAHLPLR----- 68
CC QY 61 FNEITILVWVWPFQGTDLTSCQAMF-NIOGCHLTDRSLYKNSHAVLIHHRDISW-DLT 118
CC DB 69 -----VLLWTWPFNPVALPCSEKVPKADCNITADSNVYQADAVIVHVRSHRPPM 123
CC QY 119 NLPQARPPFOKWIWMNLESPHTTPQKSGIEHNLTLTYRSDIOVPGFL-----T 172
CC DB 124 QLPPSPRPQGGORWVWFSNESFNSCLKLDLDGYFNLTNSYRSDSDIFMPYGLWLEPWSQP 183
CC QY 173 VSTNPFVEVPSKEKLVGVVSNWNPENHARVYKYNLSKSIETHYCOAPGEYVNDKNLI 232
CC DB 184 VET---LNLISAKTLKAVVSNWNTDSIRVQYKLLKPLHQLQVDVYGR-FHTPLPALMA 239
CC QY 233 PTISACKFYLSPFENSIHKDYITEKLY-NAFLAGSVVPVGLPSRENYENIPADSFIRVED 291
CC DB 240 KOLSOYKFLAFENSLHPDYITEKLRNLEAWAVPVVGLPSRVNYEQFLPPKAFIHVED 299
CC QY 292 YNSPSELAKYLKEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLDHVRHQRKYSK 349
CC DB 300 FQSPKDLAQYLLALDKDYASYLNTFRWRETLR---PRSFNLMFCKACWKLOQEPRYQT 356
CC QY 350 VGNLEKWF 357
CC DB 357 VPSIASWF 364
CC -----
CC RESULT 8
CC ID FUT6_HUMAN STANDARD; PRT; 359 AA.
CC AC P51993;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 01-MAR-2002 (Rel. 41, Last annotation update)
CC DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) Galactoside 3-L-
CC DE fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).
CC DE FUC6 OR FCT3A.
CC GN

```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92392318; PubMed=1520296;
 RA Koszidin K.L., Bowen B.R.;
 RT "The cloning and expression of a human alpha-1,3 fucosyltransferase
 capable of forming the E-selectin ligand";
 RL J. Biol. Chem. 267:24575-24584(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93077550; PubMed=1339443;
 RA Weston B.W., Smith P.L., Kelly R.J., Lowe J.B.;
 RT "Molecular cloning of a fourth member of a human alpha
 (1,3)fucosyltransferase gene family. Multiple homologous sequences
 that determine expression of the Lewis x, sialyl Lewis x, and
 difucosyl sialyl Lewis x epitopes";
 RL J. Biol. Chem. 267:24575-24584(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95378269; PubMed=7650030;
 RA Cameron H.S., Szczepaniak D., Weston B.W.;
 RT "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
 genes in normal tissues. Alternative splicing, polyadenylation, and
 isoforms";
 RL J. Biol. Chem. 270:20112-20122(1995).
 CC -1- FUNCTION: ENZYME INVOLVED IN THE BIOSYNTHESIS OF THE E-SELECTIN
 LIGAND, SIALYL-LEWIS X. CATALYZES THE TRANSFER OF FUCOSE FROM GDP-
 BETA-FUCOSE TO ALPHA-2,3 SIALYLATED SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR = GDP + 1,3-BETA-D-GALACTOSYL-
 (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER, COLON, SMALL INTESTINE,
 BLADDER, UTERUS AND SALIVARY GLAND.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M98825; AAA99222.1; -
 CC EMBL; L01698; AAB03078.1; -
 CC EMBL; U27333; AAC50192.1; -
 CC EMBL; U27334; AAC50193.1; -
 CC EMBL; U27335; AAC50194.1; -
 CC EMBL; U27336; AAC50195.1; -
 CC EMBL; U27331; AAC50190.1; -
 CC EMBL; U27332; AAC50191.1; ALT_SEQ.
 CC EMBL; U27337; AAC50196.1; -
 CC MIM; 136836; -
 CC InterPro; IPR001503; Glyco_transf_10.
 CC Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
 KW Signal-anchor; Golgi stack; Alternative splicing
 FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 35 359 LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT

FT VARSPLIC 348 359 RYQTRGIAWFT -> SSGGLIYLRLRLPEASPA (IN
 FT ISOFORM 2).
 SQ SEQUENCE 359 AA; 41859 MW; 67ABDF058F0999DA CRC64;
 Query Match 33.6%; Score 662.5; DB 1; Length 359;
 Best Local Similarity 42.88; Pred No 1.6e-42;
 Matches 133; Conservative 59; Mismatches 106; Indels 13; Caps 9;
 QY 55 STKTDYFNETIILVWVPFGQTDLTSCQAM- NIOGCHLTTRDSLYNKSHAVLIHHRDI 113
 Db 53 STGTPAHSIDPLILLWTWPNKPIALPCRCSEMPGVTADCNITADRKVYPQADAVIVHREV 112
 QY 114 SWD-LTNLPQARPFPFQKWIMNLESPTHTPQKSCIEHLENLITYRRDSIQVYCFLT 172
 Db 113 MYNPSAQLPRSPRQGRQWTFMESPSHCWQKMGDYNLTMSYRSDSDIFTYGWLE 172
 QY 173 V-STNPR--VFEVPSKEKLVWVSNWNNPHARVYKYNELSKSTEIHTYGOAFGEYNDK 229
 Db 173 PWSQPAHPPLNLISAKTELVAWVSNWGNPSARVRYQSLQAHLKVDVYGRSH-KPLPQG 231
 QY 230 NLPTISACKFYLSEFNSIHKDYITEKLY-NAFLAGSVVVLGSPSRENYENIPADSFH 288
 Db 232 TMMETLSRYKFLAFENSLHPDYITEKLRNLEAWAVPVVLGSPSRSNYERFLPPDAFIH 291
 QY 289 VEDYNSPSELAKYLKEVDKNNKLYLSYFNWRKQFTVNLPR--FWESHACIACDHWKHKQE 346
 Db 292 VDDFSQSPKDIARYLQELDKDHARYLSYFRWRETLR---PRFSWALAFCAKCKWKLQESR 348
 QY 347 YKSVGNLEKWF 357
 Db 349 YQTRG-IAWAF 358
 RESULT 9
 ID FUT3_PANTR STANDARD; PRT; 372 AA.
 AC O19038;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis
 DE alpha-4-fucosyltransferase) (Lewis Fx) (Fucosyltransferase 3) (FUCT-
 DE III) (Alpha-3/4-fucosyltransferase).
 GN FUT3.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98037800; PubMed=9368041;
 RA Costache M., Apoil P.-A., Cailleteau A., Elmgren A., Larson G.,
 RA Henry S., Blancher A., Iordachescu D., Oriol R., Mollicone R.;
 RT "Evolution of fucosyltransferase genes in vertebrates";
 RL J. Biol. Chem. 272:29721-29728(1997).
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
 INVOLVED IN THE EXPRESSION OF SIALYL LEWIS X AND LEWIS X/SEA-1
 ANTIGENS. IT MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION
 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 N-ACETYL-D-GLUCOSAMINYLR = GDP + 1,3-BETA-D-GALACTOSYL-
 (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES (A AND B). ALLELE A HAS ARG-
 162 AND VAL-304. ALLELE B HAS GLY-162 AND MET-304.
 CC -1- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL
 DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC
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 the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL; Y14033; CAA74360.1; -
 InterPro: IPR001503; Glyco_transf_10.
 Pfam: PF00852; Glyco_transf_10; 1.
 Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
 Signal-anchor; Golgi stack; Polymorphism.
 KW DOMAIN 1 14
 TRANSMEM 15 34
 (POTENTIAL).
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 LUMENAL, CATALYTIC (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 156 196
 CARBOHYD 162 162
 VARIANT R -> G (IN ALLELE B).
 V -> M (IN ALLELE B).
 SEQUENCE 372 AA; 43233 MW; 649CFB8CA7BD74C CRC64;

Query Match 33.5%; Score 560; DB 1; Length 372;
 Best Local Similarity 43.3%; Pred. No. 2.6e-42;
 Matches 130; Conservative 57; Mismatches 101; Indels 12; Gaps 8;
 QY 66 ILVWVPGQTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQQ 123
 DB 76 ILLWTFPHIPVALSRCEMVGADCHITADRKYPQADAVIVHHWDMYNPKRSLPPS 135
 QY 124 ARPPFQKWMNLESPTTPQKSGIEHLNLTLYRRSDIQVPGFLTV-STNPF--VF 180
 DB 136 PRPQSGRWIFNLEPPNCOHLEADRYFNLTMSYRSDSDIFTYPYGLWPSGQPAHPPL 195
 QY 181 EYPSKEKLVCWVSNWNNPEHARVYKYNELSKSIEHTYGOAFGEYVNDKNLPTISACKF 240
 DB 196 NLSAKTELVAWAVSNWKLDSARVRYQSLQAILKLVVDVYGRSH-KPLPKGTMTLSRYKF 254
 QY 241 YLSFENSIIHKDYITEKLY-NAFLAGSVVPVLGSPRENYENIPADSFTHVEDYNSPSLA 299
 DB 255 YLAFENSLHPDYITEKLWRNALEAWVPVVLGSPRSNYERFLPPDAFIVDDFQSPKDLA 314
 QY 300 KYLKEVDKNNKLYLYFENWRKDFTVNLRP--FWESHACIADCHVKRQYKSVGNLEKWF 357
 DB 315 RYLQELDRDHARYLYSVFRWRETLR---PRSFSWALDFCKACWKLOQESRYQTMRSIAAWF 371

RESULT 10
 ID FUT6 PANTR STANDARD; PRT; 359 AA.
 AC P56434;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).
 GN FUT6.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98037800; PubMed=9368041;
 RA Costache M., Apoll P.-A., Caillaue A., Elmgren A., Larson G.,
 RA Henry S., Blancher A., Iordachescu D., Oriol R., Mollicone R.;
 RT "Evolution of fucosyltransferase genes in vertebrates."
 RL J. Biol. Chem. 272:29721-29728(1997).
 CC -1- FUNCTION: ENZYME INVOLVED IN THE BIOSYNTHESIS OF THE E-SELECTIN
 CC LIGAND. SIALYL-LEWIS X CATALYZES THE TRANSFER OF FUCOSE FROM GDP-
 CC BETA-FUCOSE TO ALPHA-2,3 SIALYLATED SUBSTRATES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 CC N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
 CC (ALPHA-1,4-L-FUCOSYL) N-ACETYL-D-GLUCOSAMINYL-R.

-1- PATHWAY: GLYCOSYLATION.
 -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
 -1- POLYMORPHISM: THERE ARE TWO ALLELES, A AND B. ALLELE A HAS PRO-124, GLN-172 AND VAL-192. ALLELE B HAS LEU-124, GLU-172 AND ALA-192.
 -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

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EMBL; Y14033; CAA74362.1; -
 InterPro: IPR001503; Glyco_transf_10.
 Pfam: PF00852; Glyco_transf_10; 1.
 Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
 Signal-anchor; Golgi stack; Polymorphism.
 KW DOMAIN 1 14
 TRANSMEM 15 34
 (POTENTIAL).
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 LUMENAL, CATALYTIC (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 156 196
 CARBOHYD 162 162
 VARIANT R -> G (IN ALLELE B).
 V -> M (IN ALLELE B).
 SEQUENCE 372 AA; 43233 MW; 649CFB8CA7BD74C CRC64;

Query Match 33.5%; Score 559.5; DB 1; Length 359;
 Best Local Similarity 41.8%; Pred. No. 2.7e-42;
 Matches 130; Conservative 62; Mismatches 106; Indels 13; Gaps 8;
 QY 55 STKDYNETILVWVPEVPGQTDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
 DB 53 STGTPANSIPILLWTFPHIPVALSRCEMVGADCHITADRKYPQADAVIVHHREV 112
 QY 114 SWD-LTNLPQAPFPQKWMNLESPTTPQKSGIEHLNLTLYRRSDIQVPGFLT 172
 DB 113 MYNSAQPRSPRQGRWIWFSMESPSNCHLEALDGYFNLTMSYRSDSDIFTYPYGLWQ 172
 QY 173 VSTNPFV---FEVPSKEKLVCWVSNWNNPEHARVYKYNELSKSIEHTYGOAFGEYVNDK 229
 DB 173 PWSGQPVHPPLNLSAKTELVAWAVSNWGNPSARVRYQSLQAILKLVVDVYGRSH-KPLPQG 231
 QY 230 NLIPTISACKFYLSEFNSIIHKDYITEKLY-NAFLAGSVVPVLGSPRENYENIPADSFTH 288
 DB 232 TMTETLSRYKFLAFENSLHPDYITEKLWRNALEAWVPVVLGSPRSNYERFLPPDAFIH 291
 QY 289 VEDYNSPSSELAKEYLKEVDKNNKLYLYFENWRKDFTVNLRP--FWESHACIADCHVKRQ 346
 DB 292 VDDFQSPKDLARYLQELDKDHARYLYSVFRWRETLR---PRFWSALAFCKACWKLOQESR 348
 QY 347 YKSVGNLEKWF 357
 DB 349 YQT-RSIAAWF 358

RESULT 11
 ID FUT7 HUMAN STANDARD; PRT; 342 AA.
 AC Q11130;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 7) (FUCT-VII) (Selectin-ligand synthase).
 GN FUT7.

SQ	SEQUENCE	503 AA; 59159 MW; D9DA06078B6010C2 CRC64;
	Query Match	17.9%; Score 353; DB 1; Length 503;
	Best Local Similarity	32.5%; Pred. No. 3.3e-19;
	Matches	96; Conservative 42; Mismatches 105; Indels 52; Gaps
QY	88 IQCHLTTRSLYNKSHAVLIHHROTISWDLTNLPQOARPPFOKWIM--NLSPPHHTPOK 145	: : : : : : : : :
DB	202 VDTCELTANRDLASTAMILYKDHYIPTGT-----RRPSNSKQVSMLYLECPVHT-QN 254	: : : : : : : : :
QY	146 SGTEHLFNLTLYRRSDIQVPY-----GFLTVTSTNPFFVEVPSKEKLVCW 191	: : : : : : : : :
DB	255 VKYPDAINWTATYYRDSITVAPEYKWOYDFTKVQQEQDINTSVN-----KTKKVM 306	: : : : : : : : :
QY	192 VVSNWNEHARVKYYNELSKSIEIHTYGQAIFYVNDKNLIFTISAC-----KFYL 243	: : : : : : : : :
DB	307 FVSNCARGNRLOQYAHELQKYIEVDIYG-ACGNFKCSRS---TADKCFEILDNDYKFYLA 362	: : : : : : : : :
QY	244 FENSIHKDYITEKLY-NAFLAGSVPVVLGPSRENYENYIPASFIHVEDYNSPSELAKYL 302	: : : : : : : : :
DB	363 FENSNCCKDYITERFFFNALNNRVLRPLTVMGARPDEYEVSA PRSYIHVEFSSPKELAEYL 422	: : : : : : : : :
QY	303 KEVDKNNKLYSVFNKRKDFTNLPFWESHACLADCHKVRHQEYSVGNGLEKWP 357	: : : : : : : : : :
DB	423 RLIDHDDELNSYFKWKGTGEFTNTYYW----CRVCATLHNEEQLRK----PRWY 469	: : : : : : : : : :
RESULT 14	FUTC_DROME	
ID	FUTC_DROME STANDARD; PRT; 425 AA.	
AC	F83088;	
DC	01-MAR-2002 (Rel. 41, Created)	
DT	01-MAR-2002 (Rel. 41, Last sequence update)	
DT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	Alpha-(1,3)-fucosyltransferase C (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase).	
DE	FUCIC.	
GN	Drosophila melanogaster (Fruit fly).	
OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
[1]	SEQUENCE FROM N.A.	
RN	STRAIN=Canton-S;	
RC	MEDLINE=21359431; PubMed=11382750;	
RX	Adams M.D., Celiniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon K.C., Rogers Y.-H.C., Blaize R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P., Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., [2]	
RN	SEQUENCE FROM N.A.	
RN	STRAIN=Berkely;	
RC	MEDLINE=20196006; PubMed=10731132;	
RX	Adams M.D., Celiniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon K.C., Rogers Y.-H.C., Blaize R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P., Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., [2]	

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DB 316 LFDALERTVIVPVGGA--DYSRLPPHSYVDANRFMSVEGLAQYMKLVVADPDLYVSYF 373
QY 317 NWRKDFTVNLPRFWESHACIACDHV-----KRHQEKYSVGNLEKWFVN 359
DB 374 WWRSHYRLT-----YSSPFCDCARLHDPSPGHKTQFYH---DIQSWWFN 415

RESULT 15
ID FUTB_DROME STANDARD; PRT; 443 AA.
AC Q9VLCJ;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha (1,3) fucosyltransferase B (EC 2.4.1.-) (Galactoside 3-L-
DE fucosyltransferase).
GN FucB or CG4435.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RN STRAIN=Canton-S;
RN MEDLINE=21359431; PubMed=11382750;
RA Fabini G., Freilinger A., Altman F., Wilson I.B.H.;
RT "Identification of core alpha1,3-fucosylated glycans and cloning of
RT the requisite fucosyltransferase cDNA from Drosophila melanogaster;"
RT potential basis of the neural anti-horseradish peroxidase epitope.";
RL J. Biol. Chem. 276:28058-28067(2001).
RN [2]
RN SEQUENCE FROM N.A.
RN STRAIN=Berkelley;
RX MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RX Amanatides P.C., Scher S.E., Li P.-W., Roskins R.A., Galie R.F.,
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RX Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RX Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe C., Pfeiffer B.D.,
RX Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RX Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RX Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RX Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RX Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RX Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RX de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RX Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RX Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RX Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RX Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RX Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RX Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RX Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RX Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RX Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RX Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RX Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RX Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RX Nelson D.R., Nelson K.A., Niron K., Nusskern D.R., Paclet J.M.,
RX Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RX Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RX Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RX Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RX Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RX Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RX Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RX Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RX Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RX Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

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RL Science 287:2185-2195(2000).
CC -!- PATHWAY: Glycosylation.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound
CC form in trans cisternae of golgi (By similarity).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ302046; CAC41642.1; -
CC EMBL; AE003624; AAF52773.1; -
CC FLYBase; FBgn0032117; FucTB.
CC Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Signal-anchor; Golgi stack.
CC DOMAIN 1 7 27
CC TRANSMEM 7 27
CC CYTOPLASMIC (POTENTIAL).
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC LUMENAL, CATALYTIC (POTENTIAL).
CC N-LINKED (GLCNAC...) (POTENTIAL).
CC N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 436 439
CC CARBOHYD 439 439
CC CARBOHYD 439 439
CC R -> SL (IN REF. 1).
CC CONFLICT 214 214
CC CONFLICT 408 408
CC CONFLICT 416 416
CC D -> N (IN REF. 1).
CC SEQUENCE 443 AA; 51756 MW; C8FDA2CD22BFE118 CRC64;
CC
CC Query Match 12.9%; Score 254.5; DB 1; Length 443;
CC Best Local Similarity 27.9%; Pred No. 6.5e-12;
CC Matches 95; Conservative 50; Mismatches 136; Indels 57; Gaps 15;
QY 51 KNFFSTKDYFNETHILVWVWPGQTFDLTSCQAMFNQGGCHLTDRSLYNSKSHAVLIHH 110
DB 27 ENLIINENIKFNSPVELVW-WSRDSWNY-DVQRCGTHTCRITNKRSPRPWARGVLYG 84
QY 111 RDISDLTNLPOQARPPFOKWIWMNLESSTHTPQKSGIEHL--FNLTLYRDSI---- 164
DB 85 SNIKTGDFPLP---RNEHQIALLHHEESPRNTPFVSNKEFLRHFHTSTFSYSLPLTT 141
QY 165 -QVPYGLTVSTNPFV-FEVPK-----EKLYCVWVSNMNPENHARVYKYNELSKSIEHT 217
DB 142 MYLPSEALTSKDYVYVTFDGSKYGYRSTSVVFLQSCDCTMSGREDYVYKELMKHLPDS 201
QY 218 YGQAF-----GEYVND---KNLIPTISACKFYLSPENSIHKDYITEKLYNAFLAGS 265
DB 202 YGSLNRLDPERQKQDLYNNLYSPELLRFLSEYKEMIAENAAACPDYTEKFWRLMGV 261
QY 266 VPVVLG-PSRENENYIPAD-SFIHVEDYNSPELAKYLYKVDKNNKLYLSY----ENWR 319
DB 262 IPIFGSPTIKWE---PNKSAIFVNDQFQALVEYLKLNKLNKLYNSYRQHLNRR 318
QY 320 -----KDETIVNL-----PRFWESHACIACDHV 341
DB 319 NPLSNKLLHLNLTROYHIGDSSPGASLEKFECAVCYHV 358

```

Search completed: October 8, 2002, 16:52:48

Job time : 9.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:05:27 ; Search time 42.5 Seconds
(without alignments)
938.247 Million cell updates/sec

Title: US-09-744-748-1

Perfect score: 1970

Sequence: 1 MTSISKGLRFLIVCIILG.....HVKRQEVYKSVGNLEKWFVN 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	100.0	359	21	AA1980995
2	1961	99.5	359	21	AA1980996
3	693.5	35.2	405	11	AA19808119
4	693.5	35.2	405	12	AA19813752
5	693.5	35.2	405	12	AA19814404
6	693.5	35.2	405	13	AA19828840
7	693.5	35.2	530	12	AA19814405
8	689.5	35.0	405	15	AA19845937
9	689.5	35.0	405	18	AA19813641
10	685.5	34.8	405	18	AA19811821
11	679	34.5	360	18	AA19814515

12	678	34.4	360	18	AA19814514	Human chimeric fuc
13	677	34.4	361	18	AA19814530	Human chimeric fuc
14	676	34.3	361	18	AA19814520	Human chimeric fuc
15	675	34.3	361	18	AA19814517	Human chimeric fuc
16	674	34.2	360	18	AA19814516	Human chimeric fuc
17	672.5	34.1	359	18	AA19814523	Human chimeric fuc
18	672	34.1	360	18	AA19814526	Human chimeric fuc
19	672	34.1	496	15	AA19845938	A glycosyltransferase
20	671	34.1	361	18	AA19814519	Human chimeric fuc
21	670	34.0	361	12	AA19813749	GDP-Fuc:(beta-D-Ga
22	670	34.0	361	15	AA19845934	A glycosyltransferase
23	670	34.0	361	18	AA19823806	Human alpha 1,3/4
24	670	34.0	361	18	AA19814527	Human chimeric fuc
25	670	34.0	361	18	AA19813638	Human alpha(1,3)/1,
26	670	34.0	361	22	AA19864452	Human Lewis enzyme
27	670	34.0	374	15	AA19845939	A glycosyltransferase
28	670	34.0	374	18	AA19813642	Human alpha(1,3)-f
29	665.5	33.8	359	15	AA19845933	Alpha-(1-3)Fuc-TV1
30	665.5	33.8	359	18	AA19814529	Human chimeric fuc
31	665.5	33.8	359	18	AA19813643	Human alpha(1,3)-f
32	664.5	33.7	359	18	AA19814524	Human chimeric fuc
33	663.5	33.7	360	18	AA19814528	Human chimeric fuc
34	663	33.7	361	18	AA19814518	Human chimeric fuc
35	661.5	33.6	360	18	AA19814521	Human chimeric fuc
36	660.5	33.5	359	18	AA19814522	Human chimeric fuc
37	659.5	33.5	359	18	AA19814525	Human chimeric fuc
38	658.5	33.4	359	18	AA19814531	Human chimeric fuc
39	657.5	33.4	360	18	AA19814512	Human chimeric fuc
40	656.5	33.3	360	18	AA19814513	Human chimeric fuc
41	625	31.7	342	15	AA19863215	Human alpha-1,3-fu
42	622	31.6	342	20	AA19827558	Human alpha1,3-fuc
43	608.5	30.9	350	18	AA19814532	Human chimeric fuc
44	583	29.6	342	18	AA19811820	Murine myeloid-lin
45	582	29.5	342	18	AA19826671	Mouse alpha-fucosyl

ALIGNMENTS

RESULT 1
AA1980995
ID AA1980995 standard; Protein; 359 AA.
XX
AC AA1980995;
XX
DT 05-JUN-2000 (first entry)
XX
DE Murine alpha-1,3-fucosyltransferase.
XX
KW Alpha-1,3-fucosyltransferase; fucose; glycosylation; Lewis epitope;
KW brain; kidney; recombinant expression; transgenic animal; knockout
KW animal; FUC-TV; drug screening; inhibitor; potentiator; diagnosis;
KW treatment; cancer; murine; mouse.
XX
OS Mus sp.
XX
PN WO200006708-A1.
XX
PD 10-FEB-2000.
XX
PF 29-JUL-1999; 99WO-JP04092.
XX
PR 29-JUL-1998; 98JP-0213823.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Narimatsu H, Kudo T, Sasaki K;
XX
DR WPI; 2000-183120/16.
XX
DR N-PSDB; AA1982645.
XX
PT Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
epitope and an antibody recognizing it useful for diagnosis of brain

PT and kidney disease and cancer. -
 FS Claim 2; Page 121-124; 172pp; Japanese.
 XX
 CC The invention relates to a novel alpha-1,3-fucosyltransferase which
 CC transfers a fucose moiety to galactosyl-beta-1-4-N-acetylglucosamine
 CC (generating the Lewis x or y epitope). It does not transfer a fucose
 CC moiety to alpha-2,3-sialyl-galactosyl-beta-1-4-N-acetylglucosamine
 CC and therefore does not generate the sialyl-Lewis x epitope. The
 CC invention also relates to DNA sequences encoding alpha-1,3-
 CC fucosyltransferase and expression vectors and host cells comprising these
 CC DNA sequences. The invention additionally encompasses the preparation of
 CC alpha-1,3-fucosyltransferase via the culture of transformed cells or by
 CC expression of the protein in a transgenic animal; antibodies which
 CC recognise alpha-1,3-fucosyltransferase; methods for screening potential
 CC inhibitors of potential alpha-1,3-fucosyltransferase activity or
 CC expression; the preparation of compounds having fucose-containing sugar
 CC chains by use of the protein; and knockout non-human animals lacking
 CC alpha-1,3-fucosyltransferase. Alpha-1,3-fucosyltransferase has a similar
 CC substrate range to the known FUC-TIV and is expressed mainly in brain and
 CC kidney tissues. Alpha-1,3-fucosyltransferase, nucleotides which encode
 CC it, antibodies, potentiators and inhibitors may be used for the
 CC treatment and diagnosis of diseases of the brain and kidney, and of
 CC cancers. They may be used for the identification of substances
 CC which affect the activity or expression of alpha-1,3-fucosyltransferase;
 CC such substances may be used therapeutically. The knockout animals can
 CC be used to study the mechanisms of action and expression of alpha-1,3-
 CC fucosyltransferase. The present sequence represents murine
 CC alpha-1,3-fucosyltransferase.
 XX
 SQ Sequence 359 AA;
 Query Match 100.0%; Score 1970; DB 21; Length 359;
 Best Local Similarity 100.0%; Pred. No. 9 5e-171;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
 Db 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
 QY 61 FNETILVWVPFGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 Db 61 FNETILVWVPFGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 QY 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRDSIQVPYGLTVSTNPFVF 180
 Db 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRDSIQVPYGLTVSTNPFVF 180
 QY 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240
 Db 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240
 QY 241 YLSPENSIIHKDYITEKLYNAFLAGSVPLVGPSPRENYENIPADSFTHVEDFNSPSELAK 300
 Db 241 YLSPENSIIHKDYITEKLYNAFLAGSVPLVGPSPRENYENIPADSFTHVEDFNSPSELAK 300
 QY 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWESHACLDHVKRHOEYKSVGNLEKWFVN 359
 Db 301 YLKEVDKNNKLYLSYFNWRKDFTNLPRFWESHACLDHVKRHOEYKSVGNLEKWFVN 359
 RESULT 2
 AY80996
 ID AY80996 standard; Protein; 359 AA.
 XX
 AC AY80996;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Human alpha-1,3-fucosyltransferase.
 XX
 KW Alpha-1,3-fucosyltransferase; fucose; glycosylation; Lewis epitope;
 KW brain; kidney; recombinant expression; transgenic animal; knockout

KW animal; FUC-TIV; drug screening; inhibitor; potentiator; diagnosis;
 KW treatment; cancer; human.
 OS Homo sapiens.
 XX WO200006708-A1.
 XX PD 10-FEB-2000.
 XX PF 29-JUL-1999; 99WO-JP04092.
 XX PR 29-JUL-1998; 98JP-0213823.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Narimatsu H, Kudo T, Sasaki K;
 XX DR N-PSDB; AA292646, AA292647.
 XX WIPI: 2000-183120/16.
 XX DR Alpha 1,3-fucosyltransferase generating Lewis x but not sialyl-Lewis x
 PT epitope and an antibody recognizing it useful for diagnosis of brain
 PT and kidney disease and cancer. -
 XX Claim 2; Page 124-127; 172pp; Japanese.
 XX The invention relates to a novel alpha-1,3-fucosyltransferase which
 CC transfers a fucose moiety to galactosyl-beta-1-4-N-acetylglucosamine
 CC (generating the Lewis x or y epitope). It does not transfer a fucose
 CC moiety to alpha-2,3-sialyl-galactosyl-beta-1-4-N-acetylglucosamine
 CC and therefore does not generate the sialyl-Lewis x epitope. The
 CC invention also relates to DNA sequences encoding alpha-1,3-
 CC fucosyltransferase and expression vectors and host cells comprising these
 CC DNA sequences. The invention additionally encompasses the preparation of
 CC alpha-1,3-fucosyltransferase via the culture of transformed cells or by
 CC expression of the protein in a transgenic animal; antibodies which
 CC recognise alpha-1,3-fucosyltransferase; methods for screening potential
 CC inhibitors of potential alpha-1,3-fucosyltransferase activity or
 CC expression; the preparation of compounds having fucose-containing sugar
 CC chains by use of the protein; and knockout non-human animals lacking
 CC alpha-1,3-fucosyltransferase. Alpha-1,3-fucosyltransferase has a similar
 CC substrate range to the known FUC-TIV and is expressed mainly in brain and
 CC kidney tissues. Alpha-1,3-fucosyltransferase, nucleotides which encode
 CC it, antibodies, potentiators and inhibitors may be used for the
 CC treatment and diagnosis of diseases of the brain and kidney, and of
 CC cancers. They may be used for the identification of substances
 CC which affect the activity or expression of alpha-1,3-fucosyltransferase;
 CC such substances may be used therapeutically. The knockout animals can
 CC be used to study the mechanisms of action and expression of alpha-1,3-
 CC fucosyltransferase. The present sequence represents human
 CC alpha-1,3-fucosyltransferase.
 XX
 SQ Sequence 359 AA;
 Query Match 99.5%; Score 1961; DB 21; Length 359;
 Best Local Similarity 99.2%; Pred. No. 6 2e-170;
 Matches 356; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
 Db 1 MTSTSGILRPFLIVCIILGCFMACLLIYIKPTNSWVSPMESASSVLKMKNFSTKTDY 60
 QY 61 FNETILVWVPFGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 Db 61 FNETILVWVPFGQTFDLTSCQAMFNIQCHLTDRSLYKSHAVLIHHRDISWDLTNL 120
 QY 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRDSIQVPYGLTVSTNPFVF 180
 Db 121 PQARPPFKQIWMNLESPTHTPKSGIEHLFNLTLTYRRDSIQVPYGLTVSTNPFVF 180
 QY 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240
 Db 181 EVPSKEKLVCMVWVSNWNPENHARVKYNNELSKSIEHTYQAFGEYVNDKNLIPTISTCKF 240

Qy	241	YLSFENSIHKDYITEKLYNAFLAGSVVVLGFSRSENYENYPADSFIVHEDFNPSSELAK	300
Dd	241	YLSFENSIHKDYITEKLYNAFLAGSVVVLGFSRSENYENYPADSFIVHEDFNPSSELAK	300
Qy	301	YLKEVDKNKKLYLSYFNWRKDFTVNLPWFESHACIACDHYKRHOEYKSVGNLEKFWFN	359
Dd	301	YLKEVDKNKKLYLSYFNWRKDFTVNLPWFESHACIACDHYKRHOEYKSVGNLEKFWFN	359
RESULT 3			
AAR08119			
ID	AAR08119	standard; protein; 405 AA.	
XX	AAR08119;		
DT	27-FEB-1991	(first entry)	
DE	CDX, a MILA involved in ELAM1-mediated adhesion, from pCDM8 clone 7.2.		
XX	Endothelial cell-leucocyte adhesion molecule 1; ELAM1; CDX;		
KW	molecule involved in leucocyte adhesion; MILA; inflammation.		
XX	Homo sapiens.		
XX	WO9013300-A.		
PD	15-NOV-1990.		
XX	27-APR-1990;	90WO-USO2357.	
PR	18-DEC-1989;	89US-0452675.	
PR	28-APR-1989;	89US-0345151.	
PR	01-JUN-1989;	89US-0359516.	
PA	(BIOGEN INC.		
XX	Hession C, Lobb RR, Goelz SE, Born L, Benjamin CD;		
PI	Rosa MD;		
XX	WPI; 1990-361248/48.		
DR	N-PSDB; AAO06691.		
XX	Endothelial cell adhesion mols. - MILAS and DNA encoding them and inhibition-detection of binding of leukocytes to endothelial cells		
PT	Disclosure; Fig 9 (A-C); 136pp; English.		
CC	CDX is a MILA, involved in ELAM1-mediated adhesion and is probably the (or an) ELAM1 ligand. CDX is expressed in melanomas.		
CC	See also AAO06686-91.		
SQ	Sequence	405 AA;	
Query Match	35.2%;	Score 693.5; DB 11; Length 405;	
Best Local Similarity	38.8%;	Pred. No. 1.5e-54;	
Matches	154; Conservative	59; Mismatches 109; Indels 75; Gaps	
Qy	15	VCIILGCFMAC---LLIYI-----KPINSWVFSPMESASSVKMKNFSTKYTFNETILY	68
Dd	28	VCVLAAGLTCTALITYACWGOLPLPWA-SPTPS-----RPVGVL	68
Qy	69	WWPFPGOTFDL----TSCAMFNIOCHLTTRSLYNKSHAVLIHRDI-----SW----	115
Dd	69	WWEFFGGRDSAPPPDCRLRFNISCRLLTDASYGEAQAVLFHRLDLVKGPPDWPPP	128
Qy	116	-----DLNLFPQQ-----ARPFPQKWIMNLESPTHTP-QKSGIEHL	151
Dd	129	GIOAHTEAEVDLVLDYEAAAAEAALATSSPPPCQRWVMWFESPSGLSLSANL	188
Qy	152	FNLTLTTRSDIQVPYGFLTISTNPFVEVPS-----KEKLVCVVSNWNPHEARY	203

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Qy 69 WVPFGQTEFL-----TSCQAMFNIOGCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115
Db 69 WVEPFGGRDSAPRPPPCRLRFNIGSCLRLTRASYGEAQAVLFHHRDLVKGPDPWPPPW 128
Qy 116 -----DLTNLPQO-----ARPPQKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GQAHTAEVDLRVLYDEEAAAAEALATSSPPPGQORWMMNFESPSHSGLRSLASNL 188
Qy 152 FNLTLYRRSDIQVYGFELTVSTNPFVEVPS-----KEKLVCVVYNNWPEHARV 203
Db 189 FNWTLISYRADSDVPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
Qy 204 KYNELSKSIEHTYGOAF-GEYVNDKNLIPTISTCKFYLSFENSILKDKYITEKLY-NAF 261
Db 247 RYHQLSHQTVYDFVGGGPGQVPEIGLHTVARYKFLAFENSQHLDTYTEKLWRNAL 306
Qy 262 LAGSPVVLGSPRENYENYIPADSFHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDPRANYERFVRGAFIHVDDFPSASSLASLYLLFLDRNPVAVRYFHWRRS 366
Qy 322 FTVNLPFWESHACLADHVKKHQEY-KSVGNLEKWF 357
Db 367 YAVHITSFWDPEWCRVCOAVQVAGDRPKSIRNLASWF 403

RESULT 5
AAR14404
XX AAR14404 standard; Protein; 405 AA.
XX AC
XX AC
XX DT 13-FEB-1992 (first entry)
XX DE Protein 7.2 (1.3-fucosyl transferase).
XX KW CDX; cell adhesion; ELAMI.
XX OS Homo sapiens.
XX PN W09116900-A.
XX PD 14-NOV-1991.
XX PF 26-OCT-1990; 90WO-US06198.
XX PR 27-APR-1990; 90WO-US02357.
XX PR 26-OCT-1990; 90WO-US06198.
XX PA (BIOJ ) BIOGEN INC.
XX PI Goelz SE, Hession CA;
XX DR WPI; 1991-353507/48.
XX DR N-PSDB; AAQ14382.
XX DNA sequences encoding 1,3-fucosyl transferase - used to develop
XX antiinflammatory therapy by inhibition of linking activity.
XX PS Claim 23; Fig 1; 38pp; English.
XX CC The sequence was deduced from CDX pCDM8 clone 7.2 and from a
XX portion of the 7.2 insert subcloned into the sequencing vector
XX CC PN11 to prepare pSQ219. The protein, a 1,3-fucosyl transferase is
XX a surface glycoprotein which is recognised by anti-CDX antibodies
XX and which binds to ELAMI. The sequence is identical to the portion
XX CC of protein 1 (encoded by clone 1; AAQ14383) from residue 126-530.
XX CC The two proteins may represent different transcripts from the same
XX CC DNA segment. The protein may be useful in the development of anti-
XX CC inflammatory or other therapies.
XX CC See also AAR14405.
XX Sequence 405 AA;
XX

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Query Match 35.2%; Score 693.5; DB 12; Length 405;
Best Local Similarity 38.8%; Pred. No. 1.5e-54;
Matches 154; Conservative 59; Mismatches 109; Indels 75; Gaps 14;

Qy 15 VCIIILGCFMAC--LLIYI----KPTNSWVFSMESASSSVLKMKNFEFTKTDYFNETTILV 68
Db 28 VCVLAAGLGTCTALITYACWGQLPLPWA-SPTPS-----RPGVLL 68
Qy 69 WVPFGQTEFL-----TSCQAMFNIOGCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115
Db 69 WVEPFGGRDSAPRPPPCRLRFNIGSCLRLTRASYGEAQAVLFHHRDLVKGPDPWPPPW 128
Qy 116 -----DLTNLPQO-----ARPPQKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GQAHTAEVDLRVLYDEEAAAAEALATSSPPPGQORWMMNFESPSHSGLRSLASNL 188
Qy 152 FNLTLYRRSDIQVYGFELTVSTNPFVEVPS-----KEKLVCVVYNNWPEHARV 203
Db 189 FNWTLISYRADSDVPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
Qy 204 KYNELSKSIEHTYGOAF-GEYVNDKNLIPTISTCKFYLSFENSILKDKYITEKLY-NAF 261
Db 247 RYHQLSHQTVYDFVGGGPGQVPEIGLHTVARYKFLAFENSQHLDTYTEKLWRNAL 306
Qy 262 LAGSPVVLGSPRENYENYIPADSFHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDPRANYERFVRGAFIHVDDFPSASSLASLYLLFLDRNPVAVRYFHWRRS 366
Qy 322 FTVNLPFWESHACLADHVKKHQEY-KSVGNLEKWF 357
Db 367 YAVHITSFWDPEWCRVCOAVQVAGDRPKSIRNLASWF 403

RESULT 6
AAR28840
XX AAR28840 standard; Protein; 405 AA.
XX AC
XX AC
XX DT 05-APR-1993 (first entry)
XX DE HeLa cell fucosyltransferase enzyme.
XX KW glycosyltransferase; galactosyltransferase; sialyltransferase;
XX KW fucosyltransferase; membrane bound; ss.
XX OS Homo sapiens.
XX PN GB2256197-A.
XX PD 02-DEC-1992.
XX PF 14-APR-1992; 92GB-0008211.
XX PR 31-MAY-1991; 91EP-0810414.
XX PR 04-MAR-1992; 92EP-0810167.
XX PR 14-APR-1992; 92GB-0008211.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Berger EG, Meyhack B, Watzele G, Watzele M, Berger E;
XX CC WPI; 1992-401159/49.
XX DR N-PSDB; AAQ31434.
XX Glycosyltransferase prodn. process - includes transforming yeast
XX cells with expression cassettes contg. mammalian coding sequences
XX controlled by yeast promoters
XX PS Claim 16; Page 43; 65pp; English.
XX CC This sequence represents a fucosyltransferase enzyme from HeLa cells.

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XX
T T

2000

[illegible]


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PN WO9640881-A1.
XX
PD 19-DEC-1996.
XX
PF 08-MAY-1996; 96WO-US06427.
XX
PR 07-JUN-1995; 95US-0483151.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
XX Holgersson J, Seed B;
PI WPI; 1997-108639/10.
DR N-PSDB; AAT58506.
DR
XX
XX New murine alpha-(1,3)-fucosyltransferase - for fucosylating an
PT antibody to protect mammals against e.g. septic shock or septicaemia
XX
XX Claim 17; Fig 6B; 58pp; English.
XX
XX Introduction of human myeloid cell-specific fucosyltransferase
CC Fuc-TIV (AAW11821) into a murine cell line results in the appearance
CC of a fucosylated glycan pattern similar to that found on human
CC neutrophils and monocytes. Murine cells expressing human Fuc-TIV
CC show enhanced adhesion to E-selectin fusion proteins, indicating
CC that Fuc-TIV is involved in human granulocyte extravasation. Host
CC cells (e.g. 32B cl3 or human 293 cells) transformed with DNA (see
CC also AAT59506) encoding Fuc-TIV and DNA encoding murine alpha-(1,3)-
CC fucosyltransferase (see also AAW11820), can be used to fucosylate
CC ADP-antibody, IgG or IGM for use in protecting an animal against an
CC adverse immune reaction, esp. septic shock or septicaemia.
XX
XX Sequence 405 AA;
XX
Query Match 34.8%; Score 685.5; DB 18; Length 405;
Best Local Similarity 38.3%; Pred. No. 7.9e-54;
Matches 152; Conservative 60; Mismatches 110; Indels 75; Gaps 14;
QY 15 VCILGCFMAC--LLIYI-----KPTNSWFSMESASSVLKMNFFSTKTDYFNERTILV 68
Db 28 VCVLAAGLCTALITYACWGLPLFWA-SPTPS-----RPVGVLL 68
QY 69 WVPFQGTEDL-----TSCQAMENIOGCHLTDRSLYNKSHAVLIHHRDI-----SW---- 115
Db 69 WVEPFGAISAPRPPDCLRFNIGCRLLTDRASYGEAQAVLFHHRDLVKGGPDWPPPW 128
QY 116 -----DLTNLPQ-----ARPPFQKIWMNLESPTHTP-QKSGIEHL 151
Db 129 GIOHTAEVDLRLVDYEEAAAAAALATSSPRPRAKRWMMFESPSHGLRSLASNL 198
QY 152 FNTLTYYRSDSDIQVPGFLTVSTNPFVFPVS-----KEKLCVWVSVNNPHEARV 203
Db 189 FNNLTSYRADSDVFPVPGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEIHTYGOAF-GEVVDKNLPTLTSTCKEYLSFENSJHKDYITEKLY-NAF 261
Db 247 RYTHQLSQHVTVDVFGGGPGQVPEIGLHTVARVYKFLAFENSQHLDTYTEKLRNAL 306
QY 262 LAGSVPVVLGSPRENTENYIPADSFHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LACAVPVVLGPDNRANYERFVRGAFIHVDFFPSSASLASVLLFLDRNPAYVRYFHWRS 366
QY 322 FTVNLPRFWESHACLADHVKRHQEY-KSVGNLEKWF 357
Db 367 YAVHITSFWDPEWCRCVQAVORAGDRPKSIRNLASWF 403
RESULT 11
AAW14515
ID AAW14515 standard; Protein; 360 AA.
XX
AC AAW14515;
XX
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DT 19-JUN-1997 (first entry)
XX Human chimeric fucosyltransferase Fuc-TC4.
DE
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC4.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..159
FT /label= Fuc-TIV
FT /note= "amino acids 1-159 of Fuc-TIV"
FT 160..360
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT Modified-site 46
FT /label= Glycosylation
FT Modified-site 91
FT /label= Glycosylation
FT Modified-site 153
FT /label= Glycosylation
XX
PN WO9709421-A1.
XX 13-MAR-1997.
PD
XX 06-SEP-1996; 96WO-US13816.
PF
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
PT cell surface oligosaccharide structures
PT
XX
XX Claim 1; Refer to Page 294; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
CC comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
CC GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
CC enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-
CC GlcNAc alpha(1,3)-fucosyltransferase (Fuc-TVI) (AAW13643). They are
CC obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
CC (AAT61675, AAT61680) and expression in transformed host cells. The
CC chimeric fucosyltransferases can be used to modify cell surface
CC oligosaccharide structures.
XX
XX Sequence 360 AA;
XX
Query Match 34.5%; Score 679; DB 18; Length 360;
Best Local Similarity 43.1%; Pred. No. 2.6e-53;
Matches 134; Conservative 61; Mismatches 104; Indels 12; Gaps 8;
QY 55 STKTDYFNERTIILVWVPQGTEDLTSCQAMF-NIOGCHLTDRSLYNKSHAVLIHHRDI 113
Db 53 STGTPAHSIPLIILLTWTPFNKPIALPCSEMPVGTADCNITADRKVKVQADAVIVHREV 112
QY 114 SWD-LTNLPQARPPFPQKIWMNLESPTHTPQKSGIEHLNLTLYRRSDSDIQVPGFLT 172
Db 113 MYNPSAQLPSRPPRQGRWIWFSMESPSHCWQLKAMDGYENLTWSYRSDSDITFPYGLWLE 172
QY 173 V-STNPF--VFEPVSKEKLCVWVSVNNPHEARVKNYNNELSKSIEIHTYGOAFGEYNDK 229
Db 173 PWSGQPAHPPLNLAKTELVAWAVSNWKPDSARVRYYSQSLQAHLKVDVYGRSH-KPLPKG 231
QY 230 NLIPTISTCKEYLSFENSJHKDYITEKLY-NAFLAGSVPVVLGSPRENTENYIPADSFH 268
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Db 232 TMMETLSRYKYLAFENSLHPDYITEKLRNALAEAWVVPVGLPSRSNYERFLPPDAFIH 291
QY 289 VEDFNSPSELAKYLKEVDKNNKLYSYFNWRKDFTVNLP--FWESHACIACDVKRHOE 346
   || || || || || || || || || || || || || || || || || || || || ||
Db 292 VDDFQSPKDLARYLOELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLOQESR 348
QY 347 YKSVGNLEKWF 357
   || || || || || || || || || || || || || || || || || || || || ||
Db 349 YQTVRSIAAWF 359

RESULT 12
AAW14514
ID AAW14514 standard; Protein; 360 AA.
XX
AC AAW14514;
XX
DT 19-JUN-1997 (first entry)
XX
DE Human chimeric fucosyltransferase Fuc-TC3.
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC3.
XX
OS Synthetic.
XX
FH Key
FH Region 1..300
FH /label= Fuc-TIV
FH /note= "amino acids 1-300 of Fuc-TIV"
FH Region 301..360
FH /label= Fuc-TIII
FH /note= "amino acids 302-361 of Fuc-TIII"
FH Modified-site 46
FH /label= Glycosylation
FH Modified-site 91
FH /label= Glycosylation
FH Modified-site 153
FH /label= Glycosylation
XX
DN WO9709421-AL.
XX
PD 13-MAR-1997.
XX
PF 06-SEP-1996; 96WO-US13816.
XX
PR 08-SEP-1995; 95US-0525058.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Legault DJ, Lowe JB;
XX
DR WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
PS Claim 1; Refer to Page 294; 329pp; English.
XX
CC Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
CC comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
CC GlcNAc(6Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
CC enzyme) (AAW13638) and portions of the GDP-Fuc:(beta-D-Gal(1,4)-D-
CC GlcNAc alpha(1,3)-fucosyltransferase (Fuc-TVI) (AAW13643). They are
CC obcd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
CC (AA61675, AA61680) and expression in transformed host cells. The
CC chimeric fucosyltransferases can be used to modify cell surface
CC oligosaccharide structures.
XX
SQ Sequence 360 AA;

Query Match 34.4%; Score 678; DB 18; Length 360;

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Best Local Similarity 43.1%; Pred. No. 3.2e-53;
Matches 134; Conservative 60; Mismatches 105; Indels 12; Gaps 8;

QY 55 STKTDYFNETITLVWVPFGQTDLTSCQAMF-NIOGCHLTITDRSLYNKSHAVLIHHRDI 113
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Db 53 STGTPAHSIPLILLTWPFNKPIALPRCSEMVPGTADCNITADKVVYPQADAVIVHIREV 112
   || || || || || || || || || || || || || || || || || || || || ||
QY 114 SWD-LTNLPOQARPPFOKWIWMNLESPTHTPOKSGIEHLENLTLYRRSDSDIOVPYGFELT 172
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Db 113 MYNPSAQLPRSPRQGORWIFSMESPSHCWOLKAMDGYENLTMSYESDSDIPTPGWLE 172
   || || || || || || || || || || || || || || || || || || || || ||
QY 173 V-STNPF--VFEYPSKEKLYCWVWSNMNPEHARVKYNLSKLSIEIHTYCOAFGEVYNDK 229
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Db 173 PWSGQPAHPPLNLSAKTELVAWVSNWGPNSARVRYTQSQAHLKVDVYGRSH-KPLDQ 231
   || || || || || || || || || || || || || || || || || || || || ||
QY 230 NLIPTISTCKFYLSFENSIIHKDIITEKLY-NAFLAGSVVPVVLGSPSRNENYIPADSFH 288
   || || || || || || || || || || || || || || || || || || || || ||
Db 232 TMMETLSRYKYLAFENSLHPDYITEKLRNALAEAWVVPVGLPSRSNYERFLPPDAFIH 291
   || || || || || || || || || || || || || || || || || || || || ||
QY 289 VEDFNSPSELAKYLKEVDKNNKLYSYFNWRKDFTVNLP--FWESHACIACDVKRHOE 346
   || || || || || || || || || || || || || || || || || || || || ||
Db 292 VDDFQSPKDLARYLOELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLOQESR 348
   || || || || || || || || || || || || || || || || || || || || ||
QY 347 YKSVGNLEKWF 357
   || || || || || || || || || || || || || || || || || || || || ||
Db 349 YQTVRSIAAWF 359

RESULT 13
AAW14530
ID AAW14530 standard; Protein; 361 AA.
XX
AC AAW14530;
XX
DT 19-JUN-1997 (first entry)
XX
DE Human chimeric fucosyltransferase Fuc-TC19.
XX
KW Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
KW alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC19.
XX
OS Synthetic.
XX
FH Key
FH Region 1..99
FH /label= Fuc-TIII
FH /note= "amino acids 1-99 of Fuc-TIII"
FH Region 100..160
FH /label= Fuc-TVI
FH /note= "amino acids 99-159 of Fuc-TVI"
FH Region 161..361
FH /label= Fuc-TIII
FH /note= "amino acids 161-361 of Fuc-TIII"
FH Modified-site 154
FH /label= Glycosylation
XX
DN WO9709421-AL.
XX
PD 13-MAR-1997.
XX
PF 06-SEP-1996; 96WO-US13816.
XX
PR 08-SEP-1995; 95US-0525058.
XX
PA (UNMI ) UNIV MICHIGAN.
XX
PI Legault DJ, Lowe JB;
XX
DR WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
PT

```


XX PS Claim 1; Refer to Page 298; 329pp; English.

XX CC Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31) comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids (AAW1675, AAW1680) and expression in transformed host cells. The chimeric fucosyltransferases can be used to modify cell surface oligosaccharide structures.

XX SQ Sequence 361 AA;

Query Match 34.4%; Score 677; DB 18; Length 361;
Best Local Similarity 44.0%; Pred. No. 4e-53;
Matches 132; Conservative 59; Mismatches 97; Indels 12; Gaps 8;

QY 66 ILVWVPEFGTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWD-LTNLPQQ 123
DB 65 ILLWTWPFHPVALSRCEMVPGTADCHITADRKVPQADAVIHHKRVNPNFSAQLPRS 124

QY 124 ARPPFQKWIWNLESPTHTPKSGIEHLENLTLYRRSDSIQVPGFLTV-STNPF--VF 180
DB 125 PRQGGQRIWFSPHESPSCHQWQLKAMDGYFNLTMSYRSDSDIFTYPGWLEPWSGQPAHPPL 184

QY 181 EVPSKEKLVWVYNNNPEHARVYKYNELSKSIEHTYGOAFGEYVNDKNLIPTISTCKF 240
DB 185 NLSAKTELVAWVSNKPKDSARVYQSLQHLKVDVYGRSH-KPLPKGTMMETLSRYKF 243

QY 241 YLSFENSIHKDYITEKLY-NAFLAGSVPVVLPSPRENYENYIPADSFHVEDNSPELA 299
DB 244 YLAFENSLHPDYITEKLWRNALEAWAVPVVLPSPRSNRYERFLPPDAFIHVDQSPKOLA 303

QY 300 KYLKEVDKNNKLYSFNWRKDFTVNLP--FWESHACIACDHWKHOEYKSVGNLEKWF 357
DB 304 RYLQELDKDHARYLSYFRWRETLR---PRSFSWALDFCKACWKLOQESRYQTVRSIAWF 360

RESULT 14
AAW14520
ID AAW14520 standard; Protein; 361 AA.
XX AAW14520;
AC AAW14520;
XX 19-JUN-1997 (first entry)
DT Human chimeric fucosyltransferase Fuc-TC9.
XX Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
XX alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC9.
XX Synthetic.
XX Key Location/Qualifiers
FT Region 1..130
FT /label= Fuc-TIII
FT /note= "amino acids 1-130 of Fuc-TIII"
FT Region 131..160
FT /label= Fuc-TVI
FT /note= "amino acids 130-159 of Fuc-TVI"
FT Region 161..361
FT /label= Fuc-TIII
FT /note= "amino acids 161-361 of Fuc-TIII"
FT Modified-site 154
FT /label= Glycosylation
XX WO9709421-A1.
XX 13-MAR-1997.
XX

PF 06-SEP-1996; 96WO-US13816.
XX 08-SEP-1995; 95US-0525058.
PR (UNMI) UNIV MICHIGAN.
XX Legault DJ, Lowe JB;
PI WPI; 1997-192897/17.
XX New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
PT Claim 1; Refer to Page 295; 329pp; English.
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31) comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis enzyme) (AAW13638) and portions of the GDP-Fuc:beta-D-Gal(1,4)-D-GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids (AAW1675, AAW1680) and expression in transformed host cells. The chimeric fucosyltransferases can be used to modify cell surface oligosaccharide structures.

XX SQ Sequence 361 AA;

Query Match 34.3%; Score 676; DB 18; Length 361;
Best Local Similarity 43.8%; Pred. No. 4.9e-53;
Matches 133; Conservative 56; Mismatches 95; Indels 20; Gaps 9;

QY 66 ILVWVPEFGTDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
DB 65 ILLWTWPFHPVALSRCEMVPGTADCHITADRKVPQADTVIVHH---WDIWSNPKSR 120

QY 120 LPQARPPFQKWIWNLESPTHTPKSGIEHLENLTLYRRSDSIQVPGFLTV-STNPF 178
DB 121 LPSPRQGGRIWFSPHESPSCHQWQLKAMDGYFNLTMSYRSDSDIFTYPGWLEPWSGQPA 180

QY 179 --VFEVPSKEKLVWVYNNNPEHARVYKYNELSKSIEHTYGOAFGEYVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELVAWVSNKPKDSARVYQSLQHLKVDVYGRSH-KPLPKGTMMETLS 239

QY 237 TCKFYLSFENSIHKDYITEKLY-NAFLAGSVPVVLPSPRENYENYIPADSFHVEDNSP 295
DB 240 RYKELYAFENSLHPDYITEKLWRNALEAWAVPVVLPSPRSNRYERFLPPDAFIHVDQSP 299

QY 296 SELAKYLKEVDKNNKLYSFNWRKDFTVNLP--FWESHACIACDHWKHOEYKSVGNL 353
DB 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRSFSWALDFCKACWKLOQESRYQTVRSI 356

QY 354 EKWF 357
DB 357 AAWF 360

RESULT 15
AAW14517
ID AAW14517 standard; Protein; 361 AA.
XX AAW14517;
AC AAW14517;
XX 19-JUN-1997 (first entry)
DT Human chimeric fucosyltransferase Fuc-TC6.
XX Alpha(1,3/1,4)-fucosyltransferase; Lewis enzyme; Fuc-TIII;
XX alpha(1,3)-fucosyltransferase; Fuc-TVI; glycosylation;
KW oligosaccharide; Fuc-TC6.
XX Synthetic.
XX Key Location/Qualifiers
FH

Job time : 43.5 secs

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FT Region 1..70
FT /label= Fuc-TIII
FT /note= "amino acids 1-70 of Fuc-TIII"
FT 71..86
FT /label= Fuc-TVI
FT /note= "amino acids 70-85 of Fuc-TVI"
FT 87..361
FT /label= Fuc-TIII
FT /note= "amino acids 87-361 of Fuc-TIII"
FT 154
FT /label= Glycosylation
XX
XX WO9709421-A1.
XX
XX 13-MAR-1997.
XX
XX 06-SEP-1996; 96WO-US13816.
XX
XX 08-SEP-1995; 95US-0525058.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Legault DJ, Lowe JB;
XX
XX WPI; 1997-192897/17.
XX
XX New recombinant fucosyltransferase proteins - useful for modifying
XX cell surface oligosaccharide structures
XX
XX Claim 1; Refer to Page 295; 329pp; English.
XX
XX Chimeric fucosyltransferases Fuc-TC1 to Fuc-TC21 (AAW14512-31)
XX comprise portions of the human GDP-Fuc:(beta-D-Gal(1,4/1,3))-D-
XX GlcNAc(Glc) alpha(1,3/1,4)-fucosyltransferase (Fuc-TIII, Lewis
XX enzyme) (AAW13638) and portions of the GDP-Fuc:(beta-D-Gal(1,4)-D-
XX GlcNAc alpha(1,3)fucosyltransferase (Fuc-TVI) (AAW13643). They are
XX obtd. by cassette mutagenesis of Fuc-TIII and Fuc-TVI nucleic acids
XX (AAW61675, AAW61680) and expression in transformed host cells. The
XX chimeric fucosyltransferases can be used to modify cell surface
XX oligosaccharide structures.
XX
XX Sequence 361 AA;

Query Match 34.38; Score 675; DB 18; Length 361;
Best Local Similarity 43.48; Pred. No. 6.1e-53;
Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;

Qy 66 ILVWVWPGQFTDLSQAMF-NIQGCHLTDRSLYKSHAVLIHHRDISWDL-----TN 119
Db ||| ||| : | | | ||| ||| : | | | ||| : | | | ||| :
Qy 120 LPOQARPPQKWIWNLESPTHPTQKSGIEHLENTLTYYRRSDIQVYGFV-STNPF 178
Db || || ||| ||| : | | | ||| ||| : | | | ||| ||| : |
Qy 121 LPPSPRQGWIFNLEPPPCQHLAALDRYFNLTMYSRSDSDIPTYGWLEPWSGQA 180
Db || ||| ||| : | | | ||| ||| : | | | ||| ||| : |
Qy 179 --VEEVPSEKLVGVVSNWNPHEHARVYKYNELSKSIEIHTYQAGFGEYVNDKNLIPTIS 236
Db : | : | | | | | | | | | | | | | | : | : | : | : |
Qy 181 HPPLNLSAKTELVAWVSNWNPDSARVRYGSLQAHKVDVYGRSH-KPLPKGTMMETLS 239
Db
Qy 237 TCKEVLSPENSIHKDYTEKLY-NAFLAGSVPVVLGSPRENYENYIPADSFIVHEDENSP 295
Db ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Qy 240 RYKFLAFENSLHPDYITEKLRNLEAWAVPVVLGSPRSNYERFLPDAFIHVDDEQSP 299
Db
Qy 296 SELAKYLVKVDKNNKLYSYNWKDKFTVNLPR--FWESHACIACDVKKHQQEYKSGVNL 353
Db : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
Qy 354 EKWF 357
Db ||
Qy 357 AAWF 360
Db ||

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 16:34:47 ; Search time 15.5 Seconds
(without alignments)
2225.553 Million cell updates/sec

Title: US-09-744-748-1
Perfect score: 1970
Sequence: 1 WTSTSGILRFLIVCIILG.....HVKRHQEYKSVGNLEKWFVN 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR71:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	35.8	433	2 A57596	alpha-1,3-fucosylt
2	698	35.4	400	2 JC4591	alpha-1,3 fucosylt
3	693.5	35.2	405	2 B36340	alpha(1,3)-fucosyl
4	670	34.0	361	2 A36669	galactoside 3(4)-L
5	670	34.0	374	2 A42270	alpha (1,3) fucosyl
6	665.5	33.8	359	2 A45156	alpha-(1,3)-fucosyl
7	657	33.4	365	2 S53498	alpha(1,3/4)-fucos
8	650	33.0	364	2 I39048	alpha (1,3) fucosyl
9	622	31.6	342	2 A54057	alpha(1,3)-fucosyl
10	478.5	24.3	304	2 I39049	alpha (1,3) fucosyl
11	307	15.6	414	2 T15270	hypothetical prote
12	304	15.4	1652	2 T18799	hypothetical prote
13	285.5	14.5	451	2 T23491	hypothetical prote
14	227.5	11.5	393	2 H96742	hypothetical prote
15	204.5	10.4	513	2 F96533	probable fucosyltr
16	156.5	7.9	183	2 C97832	alpha-(1,3)-fucosyl
17	154.5	7.8	346	2 T44327	hypothetical prote
18	133.5	6.8	425	2 C64567	fucosyltransferase
19	133	6.8	436	2 G71862	alpha-(1,3)-fucosyl
20	133	6.8	454	2 B71914	alpha (1,3)-fucosyl
21	131.5	6.7	476	2 C64601	fucosyltransferase
22	124.5	6.3	876	2 S71277	serine/threonine-s
23	124.5	6.3	876	2 D85350	hypothetical prote
24	115.5	5.9	682	2 F81332	probable periplasm
25	114	5.8	1088	2 T41671	hypothetical prote
26	108	5.5	2628	2 S59413	probable membrane
27	105	5.3	537	2 T21823	hypothetical prote
28	104	5.3	747	2 T33488	hypothetical prote
29	102	5.2	2059	2 T41933	large tegument pro

30	100.5	5.1	382	2 T29554	hypothetical prote
31	99.5	5.1	789	2 G90587	lipoprotein [impor
32	99	5.0	2028	2 T08025	DNA-directed RNA p
33	99	5.0	4550	2 T18440	hypothetical prote
34	98	5.0	441	2 F84560	purple acid phosph
35	98	5.0	526	2 F82873	hypothetical prote
36	97.5	4.9	335	2 AD1880	hypothetical prote
37	97.5	4.9	354	2 B97003	spermidine/putresc
38	97	4.9	408	2 T47585	hypothetical prote
39	97	4.9	1253	2 T40302	hypothetical prote
40	96.5	4.9	530	2 G71157	hypothetical prote
41	96.5	4.9	759	2 I38593	fibroblast activat
42	96	4.9	321	2 S54403	1-phosphatidylinos
43	96	4.9	566	2 JH0218	cellulase (EC 3.2.
44	96	4.9	1092	1 S37676	glutamate dehydrog
45	95.5	4.8	370	2 JC7591	spinal cord-derive

ALIGNMENTS

RESULT 1

A57596
alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - mouse
N:Alternate names: ELAM-1 ligand fucosyltransferase homolog
C:Species: Mus musculus (house mouse)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 11-Jan-2000
C:Accession: A57596
R:Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.;
J. Biol. Chem. 270, 25047-25056, 1995
A:Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific e
rase.
A:Reference number: A57596; MUID:96027607
A:Accession: A57596
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <ER>
A:Cross-references: GB:U33457; NID:gl039426; PTDN:AAC52269.1; PID:gl039427
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 35.8%; Score 706; DB 2: Length 433;
Best Local Similarity 42.7%; Pred. No. 9.4e-46;
Matches 146; Conservative 48; Mismatches 96; Indels 52; Gaps 8;

QY	66	ILVVMWPF-----GQTFDLTSCQAMFNIQGCGLTDRSLYKNSHAVLIHRDISWDLTNLP	121
DB	92	VLLWEPFRGCGYPKSPDCLSRFNISGCRLLTDRAAYGEAQAVLFHRLDYKELHDWP	151
QY	122	QQ-----ARPPFQKWIWNLESPTHTPKSG	147
DB	152	PPWGARERTDKALVLRVDFDQEGAVTLTGKALETVGSRPPCQRVWVWVNFESPSHTPLRG	211
QY	148	I-EHLNLTITRRSDIOVPGFLTVSTNPFVFEVPS-----KEKLVGVVWSNWP	198
DB	212	LAKDLNWTUSYTDSDVFPYGLYRSRDP--TEQPSGLGPGQLARRRGLVAVWVWSNNE	269
QY	199	EHARVYNNELSKSIETHTYQCAF-GEYVNDKNLPISTCKFVLSFENSHTKDYITEKL	257
DB	270	HQARVRYHQLSRHVSVDVFGRTGPRVPAIGLLHTVARYKFLAFENSRHVDYITEKL	329
QY	258	Y-NAFLAGSVPVVLGSPRENYENYIPADSIHVEDFNPSSELAKEYKVDKNKLYLSYF	316
DB	330	WRNAFLAGAVPVVGLGPDRAHYERFVRPGAFTHVDDDFPNAASLAAYLLFLDRNVAVRYRF	389
QY	317	NWRKDTVNLPRFWEHSHACLDHVKRH-QEYKSVGNLEKWF	357
DB	390	RWRSEAVHITSEWDEQWCRTCAQVOTSGDQPKSIHNLADWF	431

RESULT 2

JC4591
alpha-1,3 fucosyltransferase (EC 2.4.1.-) - mouse

[illegible]

A:Accession: I39050
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U27333; NID:9967202; PIDN:AAC50192.1; PID:9967203
A:Accession: I39051
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE2>
A:Cross-references: EMBL:U27334; NID:9967204; PIDN:AAC50193.1; PID:9967205
A:Accession: I39052
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: EMBL:U27335; NID:9967206; PIDN:AAC50194.1; PID:9967207
A:Accession: I39053
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE4>
A:Cross-references: EMBL:U27336; NID:9967208; PIDN:AAC50195.1; PID:9967209
A:Accession: I39054
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <RE5>
A:Cross-references: EMBL:U27337; NID:9967210; PIDN:AAC50196.1; PID:9967211
C:Genetics:
A:Gene: GDB:FUT6
A:Cross-references: GDB:135180; OMIM:136836
A:Map position: 19p13.3-19p13.3
A:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase
Query Match 33.8%; Score 665.5; DB 2; Length 359;
Best Local Similarity 43.1%; Pred. No. 8.4e-43;
Matches 134; Conservative 58; Mismatches 106; Indels 13; Gaps 9;
QY 55 STKDYFNETHILVWVWPGQFDTLSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDI 113
DB 53 STGTFAHSIPLLLTWTFPNKPIALPCSEMVPGTADCNITADRKVYQADAVIVHREV 112
QY 114 SWD-LTNLPQARPPFKQKWNLESPTHTPOKSGIEHLNLTITRYRDSDIQVPGFLT 172
DB 113 MYNSAQLPFRPQGGQWIFWSESFSCWOLKAMDGYFNLMTSYRSDSDIFTPYGNLE 172
QY 173 V-STNPF--VFEVPSKEKLVWVSNWNPENHARVYKYNELSKSIEHTYQAGFGEVYNDK 229
DB 173 PWSGQAPHPPLNLSAKTELVAWVSNWNPENHARVYKYNELSKSIEHTYQAGFGEVYNDK 231
QY 230 NLPTISTCKFYLSFENSITKDYITEKLY-NAFLAGSVVPLGSPRENYENIPADSFTH 288
DB 232 TMWETLSRYKFLAFENSLHPDYITEKLNALQAWAVPVVLGSPRVNYEQFLPKAFTHVED 299
QY 289 VEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLADCHVRRHQE 346
DB 292 VDDFQSPKDLARYLQELDKDHARYLSYFWRWRETLR---PRSFSWALAFCKACWKLBESR 348
QY 347 YKSVGNLEKWF 357
DB 349 YQTRG-IAAWF 358
RESULT 7
S55498
alpha(1,3/4)-fucosyltransferase - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 13-Sep-1998
A:Accession: S55498
R:Oulmouden, A.; Wierincx, A.; Petit, J.M.; Julien, R.
submitted to the EMBL Data Library, June 1995
A:Description: Molecular cloning and expression of bovine alpha (1.3/4)-fucosyltransferase
A:Reference number: S55498
A:Accession: S55498
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-365 <OUL>
A:Cross-references: EMBL:X87810; NID:9860807; PID:9860808
C:Superfamily: galactoside 3(4)-L-fucosyltransferase
Query Match 33.4%; Score 657; DB 2; Length 365;
Best Local Similarity 38.9%; Pred. No. 3.8e-42;
Matches 143; Conservative 66; Mismatches 117; Indels 42; Gaps 12;
QY 11 PFLIVCIILG-CFMACLLI---YIKPTNSWV-----FSPMESASSVLKMKNFSTKTDY 60
DB 18 PGLLLQALLALCFYSYLRMSQEKPKPMWVSELGAPSQATEGSSAHLPLR----- 68
QY 61 ENETTILVWVWPGQFDTLSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISW-DLT 118
DB 69 -----VLLTWTFPNQVALSRCELPWGTADCOLTVNRSEYFQADAVFVHREVSHRPMK 123
QY 119 NLPQOARPPFKQKWNLESPTHTPOKSGIEHLNLTITRYRDSDIQVPGFLT-----T 172
DB 124 QLPSPRPADQWVWFSMESPSNCLAKDLGDYFNLTMTSYRSDSDIFTPYGNLEPWSQP 183
QY 173 VSTNPFVFEVPSKEKLVWVSNWNPENHARVYKYNELSKSIEHTYQAGFGEVYNDKNI 232
DB 184 VET---LLNLSAKTLVAWVSNWNPENHARVYKYNELSKSIEHTYQAGFGEVYNDKNI 239
QY 233 PTISTCKFYLSFENSITKDYITEKLY-NAFLAGSVVPLGSPRENYENIPADSFTHVED 291
DB 240 KQLSOYKFLAFENSLHPDYITEKLNALQAWAVPVVLGSPRVNYEQFLPKAFTHVED 299
QY 292 FNSPSELAKYLKEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLADCHVRRHQEYKS 349
DB 300 FQSPKDLAQVLLALDKDYASLYNFWRETLR---PRSFSWALMECKACWKLBQEPRIQT 356
QY 350 VGNLEKWF 357
DB 357 VPSIASMF 364
RESULT 8
I39048
alpha(1,3) fucosyltransferase FUT6-related splice form I - human
C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 29-Sep-1999
C:Accession: I39048
R:Camaron, H.S.; Szczepaniak, D.; Weston, B.W.
J. Biol. Chem. 270, 20112-20122, 1995
A:Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in no
A:Reference number: I39043; MUID:95378269
A:Accession: I39048
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364 <RES>
A:Cross-references: EMBL:U27331; NID:9967198; PIDN:AAC50190.1; PID:9967199
C:Genetics:
A:Gene: GDB:FUT6
A:Cross-references: GDB:135180; OMIM:136836
A:Map position: 19p13.3-19p13.3
A:Superfamily: galactoside 3(4)-L-fucosyltransferase
C:Keywords: alternative splicing
Query Match 33.0%; Score 650; DB 2; Length 364;
Best Local Similarity 44.5%; Pred. No. 1.3e-41;
Matches 130; Conservative 53; Mismatches 97; Indels 12; Gaps 8;
QY 55 STKDYFNETHILVWVWPGQFDTLSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDI 113
DB 53 STGTFAHSIPLLLTWTFPNKPIALPCSEMVPGTADCNITADRKVYQADAVIVHREV 112
QY 114 SWD-LTNLPQARPPFKQKWNLESPTHTPOKSGIEHLNLTITRYRDSDIQVPGFLT 172
DB 113 MYNSAQLPFRPQGGQWIFWSESFSCWOLKAMDGYFNLMTSYRSDSDIFTPYGNLE 172
QY 173 V-STNPF--VFEVPSKEKLVWVSNWNPENHARVYKYNELSKSIEHTYQAGFGEVYNDK 229
DB 173 PWSGQAPHPPLNLSAKTELVAWVSNWNPENHARVYKYNELSKSIEHTYQAGFGEVYNDK 231
QY 230 NLPTISTCKFYLSFENSITKDYITEKLY-NAFLAGSVVPLGSPRENYENIPADSFTH 288
DB 232 TMWETLSRYKFLAFENSLHPDYITEKLNALQAWAVPVVLGSPRVNYEQFLPKAFTHVED 299
QY 289 VEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLADCHVRRHQE 346
DB 292 VDDFQSPKDLARYLQELDKDHARYLSYFWRWRETLR---PRSFSWALAFCKACWKLBESR 348
QY 347 YKSVGNLEKWF 357
DB 349 YQTRG-IAAWF 358
RESULT 7
S55498
alpha(1,3/4)-fucosyltransferase - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 13-Sep-1998
A:Accession: S55498
R:Oulmouden, A.; Wierincx, A.; Petit, J.M.; Julien, R.
submitted to the EMBL Data Library, June 1995
A:Description: Molecular cloning and expression of bovine alpha (1.3/4)-fucosyltransferase
A:Reference number: S55498
A:Accession: S55498
A:Status: preliminary

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Db 173 PWSQPAHPPLNLSAKTELAVAWSNWGNPSARVRYQSLQAHLKVDVYGRSH-KPLPQG 231
QY 230 NLPTISTCKFYLSFENSIIHKDYTEKLY-NAFLAGSVPPVVLGSPSRENYENYIPADSFIIH 288
Db 232 TMMETLSRYKRYLAFENSLHPDYITTEKLWRNALEAWAVPVVLGSPSRSNYERFLPPDAFIIH 291
QY 289 VEDFNSPSELAKYLKEVDKNNKLYLSYFNWRKDFVTNLP--FWESHACIAC 338
Db 292 VDDFQSPDLARLYQLQELDKDHARYLSYFRWRETLR---PRFSWALAFCKAC 340

RESULT 9
A54057
alpha(1,3)-fucosyltransferase (EC 2.4.1.-) 7 precursor - human
N;Alternate names: leukocyte fucosyltransferase FucTVII
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 20-Apr-2000
C;Accession: A54057; A53713
R;Sasaki, K.; Kurata, K.; Funayama, K.; Nagata, M.; Watanabe, E.; Ohta, S.; Hanai, N.; J. Biol. Chem. 269, 14730-14737, 1994
A;Title: Expression cloning of a novel alpha(1,3)-fucosyltransferase that is involved in B cell development
A;Reference number: A54057; MUID:94237894
A;Accession: A54057
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-342 <SAS>
A;Cross-references: GB:X78031; NID:g516292; PIDN:CAA54962.1; PID:g516293
R;Natsuka, S.; Gersten, K.M.; Zenita, K.; Kannagi, R.; Lowe, J.B. J. Biol. Chem. 269, 16789-16794, 1994
A;Title: Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase
A;Reference number: A53713; MUID:94266898
A;Accession: A53713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-160,'A',163-303,'SV',306-342 <NAT>
A;Cross-references: GB:U08112; NID:g520463; PIDN:AAA56869.1; PID:g520464
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:373982
A;Map position: 9pter-9qter
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-342/Product: alpha(1,3)-fucosyltransferase 7 #status predicted <NAT>
F;81,291/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.6%; Score 622; DB 2; Length 342;
Best Local Similarity 43.3%; Pred. No. 1.5e-39;
Matches 130; Conservative 48; Mismatches 108; Indels 14; Gaps 8;

QY 65 TILVWVWPF-GQTFDLTS--CQAMFNIGCHLTDRSLYNKSHAVLIHHRDISWDLTNLP 121
Db 48 TILVWVWPFDDQPELPSDTC-TRYGIARCLSANRSLASADAVVPHRELQTRRSHLP 106
QY 122 QQARPPPKKWIWNLESPTTPQKSGIEHLFNLTLYTTRSDIOVPGFLTVSTNPPVFE 181
Db 107 LAQPRGQPVWVWASMSPSHTGLSHLURGIIFNWLVSRYRSDIDIFVPYGLRPHWGSP-P 165
QY 182 VPSEKILVCVWVSNWNPPEHARVYNNLSKSIETHTYQAFGEYVNDKNIPTISTCKFY 241
Db 166 LPAKSRVAWVSNFQERQLRRLYRQLAPHLRVDVFGNRPCLASCIVPIVAQYRFY 225
QY 242 LSFENSTHKDYITEKLY-NAFLAGSVPPVVLGSPSRENYENYIPADSFTHVEDFNSPSLAK 300
Db 226 LSFENSQHRDYITEKFNALVALAGTVPVLGPPRATVEAFVPADAFVHVDVDFGSARELAA 285
QY 301 YLKEVDKNNKLYLSYFNWRKDFVTNLP--FWESHACIACD---HVKKRQYKSVGNLEKWF 357
Db 286 FL--TGMNESYQRFFAWRDLRLVRLFTDRERFCAICDRPHLPQRSQVYE---DLEGWF 340

RESULT 10
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```
I39049
alpha(1,3) fucosyltransferase FUT6-related splice form II - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 29-Sep-1999
C;Accession: I39049
R;Cameron, H.S.; Szczepaniak, D.; Weston, B.W. J. Biol. Chem. 270, 20112-20122, 1995
A;Title: Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in no
A;Reference number: I39043; MUID:95378269
A;Accession: I39049
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-304 <RES>
A;Cross-references: EMBL:U27332; NID:g967200; PIDN:AAC50191.1; PID:g967201
C;Genetics:
A;Gene: GDB:FUT6
A;Cross-references: GDB:135180; OMIM:136836
A;Map position: 19p13.3-19p13.3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: alternative splicing

Query Match 24.3%; Score 478.5; DB 2; Length 304;
Best Local Similarity 43.0%; Pred. No. 9e-29;
Matches 98; Conservative 42; Mismatches 81; Indels 7; Gaps 6;

QY 55 STKTDYFNETTILVWVWPFQTFDLTSCQAMF-NIQCHLTDRSLYNKSHAVLIHHRDI 113
Db 53 STGTPAHSIFLILTLWTPFNKPIALPRCSEMFPTADCNITADRKVYPQADAVIVHREV 112
QY 114 SWD-LTNLPOQARPPQKWKWMLNLESTHTPQKSGIEHLFNLTLYTTRSDIOVPGFLT 172
Db 113 MYNPSAQLPRSPRQQRWLFWSMESPSHCQWLKAMDGYFNLTWYSRSDSDIFTPTYGWLE 172
QY 173 V-STNPF--VFEVPSKEKLYCVWVSNWNPPEHARVYNNLSKSIETHTYQAFGEYVNDK 229
Db 173 PWSQPAHPPLNLSAKTELAVAWSNWGNPSARVRYQSLQAHLKVDVYGRSH-KPLPQG 231
QY 230 NLPTISTCKFYLSFENSIIHKDYTEKLY-NAFLAGSVPPVVLGSPSREN 276
Db 232 TMMETLSRYKRYLAFENSLHPDYITTEKLWRNALEAWAVPVVLGSPSRN 279

RESULT 11
T15270
hypothetical protein F59E12.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: T15270
R;Johnson, D.
Submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E12.
A;Reference number: Z18318
A;Accession: T15270
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-414 <OJH>
A;Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088845; PIDN:AAB54261.1; GSPD:
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
A;Gene: CESP:F59E12.13
A;Map position: 2
A;Introns: 90/3; 237/2; 279/3; 309/2; 339/2; 388/3
C;Superfamily: galactoside 3(4)-L-fucosyltransferase

Query Match 15.6%; Score 307; DB 2; Length 414;
Best Local Similarity 27.7%; Pred. No. 1.2e-15;
Matches 97; Conservative 59; Mismatches 120; Indels 74; Gaps 17;

QY 66 ILVWVWPFQTFD---LTSCQAMFNIGCHLTDRSLYNKSHAVLIHHRDISWDLTNLP- 121
Db 67 ILVWTTTFGATVPSTALSDCPGL--TDRCVIDTNRHQLDSADAVVFAADIS----KFPL 120
QY 122 QQARPPPKKWIWNLESPTTPQKSG-----IEHLFNLTLYTTRSD 163
```



```
Db 122 -CLWTKSSVLADSPDALLFETTTPLQRRVGDPLRVYMELEAGR---KRSREDIF--I 174
QY 157 TYRDSIDIQVPYGFELVSNPFVEPSK--EKLYCWVSNWNPENHARVYKYNELSKS-- 212
Db 175 SYHAKDDVQTTAGSLFHNHNNYHISPHKNNNDVLVYSSSRCLPHRDR-----LAKSL 228
QY 213 --IEIHTYGA-----FGEYNDKN-----LIPTISTCKFYLSFENSIH 249
Db 229 DLIPHISFGKCLNNVGLDSALSMYECVAENHNAEKWDLHLCAMSHYKFVLAIENTAV 288
QY 250 KQYTEKLYNFIAGSVVVLGSPRENYENIPADSFHVEDFNSPSELAKYLKEVDKNN 309
Db 289 ESYVTEKLFALDGSVPYIFGAS--NVQDFVPPHSDVIGSKFGSMQELAAAYVKRLGDDP 346
QY 310 KLYLSYFNWR-----KDFVNLPRFWESHACIADHVKR 343
Db 347 VAYSEYHAMRRCLMGNYGKTRAVSL-----DTLPCRICEISR 385

RESULT 15
F96533
Probable fucosyltransferase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96533
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F96533
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: GB:AE005173; NID:g10120428; PIDN:AAG13053.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14J22.8
A:Map position: 1

Query Match 10.4%; Score 204.5; DB 2; Length 513;
Best Local Similarity 25.7%; Pred. No. 9.2e-08;
Matches 77; Conservative 50; Mismatches 122; Indels 51; Gaps 15;

QY 56 TKTDYFNEITILYVWVFGTFLTSCQ---AMFNIGQH---LTTDRSLYNKSHA--V 106
Db 70 TLTDFFTQSPSL-----SQSPPARSDRKKIGLFTDRSCCEWLMREDSVTYSRDTKDPI 123
QY 107 LIH--HRDISW---DLT-----NLPOQA---RPPFKWIWNLESPTHPOKSGIEHL 151
Db 124 FISGGKDFQWCSDCTFGDSSGKTDAAFGLGCKFGTGLSIIRSMESAQYYPEN----- 177
QY 152 FNLTLYRDSOI-----QVPYGLVSTNPFVFEV-PSKEKLVCVW-VSNWNPEHA 201
Db 178 -DLAQARRRGYDIVMTTSLSSDVPVGFYSWAEYDINSVPQKTERAIAAFAISNCGARNF 236
QY 202 RVKYYNELSK-STEIHTYGAQGEYNDKNLIPTISTCKFYLSFENSIHKDYITEKLYNA 260
Db 237 RLQALEALMKTNIKIDSYGGCHNRDGVKDVKVEALKRYKFSLAFENTNEEDYVTEKFFQS 296
QY 261 FLAGSPVVLGSPRENYENIPA-DSFIHVEDFNSPSELAKYLKEVDKNNKLYLSYFNWR 319
Db 297 LVAGSPVWVVGPP--PNIEEPAPASDSFLIKHTMEDVEPVAKRMKYLAAAPAAYNQTLRWK 354
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Search completed: October 8, 2002, 16:54:35

Job time : 18.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 8, 2002, 15:06:57 ; Search time 8.5 Seconds
(without alignments)
1635,332 Million cell updates/sec

Title: US-09-744-748-1
Perfect score: 1970
Sequence: 1 MFTSTKGIILRPFLIVCIILG.....HVKRHQEKSVGNLEKWFVN 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	35.8	433	1	FUT4_MOUSE
2	694.5	35.3	433	1	FUT4_RAT
3	691.5	35.1	405	1	FUT4_HUMAN
4	670	34.0	361	1	FUT3_HUMAN
5	670	34.0	374	1	FUT5_HUMAN
6	669	34.0	365	1	FUT3_BOVIN
7	669	34.0	374	1	FUT5_PANTR
8	665.5	33.8	359	1	FUT6_HUMAN
9	663	33.7	372	1	FUT3_PANTR
10	662.5	33.6	359	1	FUT6_PANTR
11	622	31.6	342	1	FUT7_HUMAN
12	582	29.5	389	1	FUT7_MOUSE
13	356	18.1	503	1	FUTA_DROME
14	297.5	15.1	425	1	FUTB_DROME
15	257.5	13.1	443	1	FUTC_DROME
16	227.5	11.5	401	1	FUL3_ARATH
17	204.5	10.4	513	1	FUL2_ARATH
18	200	10.2	501	1	FUL1_ARATH
19	105	5.3	537	1	UGT5_CABEL
20	102	5.2	2059	1	TEGU_HSV7J
21	101	5.1	663	1	GRIA_BACCE
22	100.5	5.1	638	1	Y153_HUMAN
23	100	5.1	810	1	Z33A_HUMAN
24	98.5	5.0	623	1	RPOC_GUITH
25	96	4.9	566	1	GUNC_PABLA
26	96	4.9	1092	1	DHE2_YEAST
27	95	4.8	1480	1	CFTR_HUMAN
28	94	4.8	678	1	GSHL_YEAST
29	93.5	4.7	781	1	HELL_HSVSA
30	93.5	4.7	986	1	EP1B_STAEP
31	93	4.7	387	1	CXY_CLOS
32	91.5	4.6	1147	1	NRDC_HUMAN
33	91.5	4.6	1173	1	NIFU_ENTAG

34	91	4.6	398	1	SPEB_STRPY	P00788 streptococ
35	91	4.6	734	1	METE_THEMA	Q9112 thermotoga
36	91	4.6	772	1	LP1G_DROME	PI197 drosophila
37	90.5	4.6	584	1	MUTL_BUCAI	P57633 buchnera ap
38	90	4.6	921	1	DPOI_RICHE	Q91156 rickettsia
39	90	4.6	6669	1	NEBU_HUMAN	P20929 homo sapien
40	89.5	4.5	934	1	SVLL_SULSO	P58176 sulfolobus
41	89	4.5	378	1	MNT3_CANAL	P87207 candida alb
42	89	4.5	438	1	RGSB_MOUSE	Q922h1 mus musculus
43	89	4.5	471	1	CD36_BOVIN	P26201 bos taurus
44	89	4.5	2352	1	MOKC_SCHPO	Q9uul4 schizosacch
45	88.5	4.5	372	1	Y983_CAWJE	P45492 campylobact

ALIGNMENTS

RESULT 1						
FUT4_MOUSE						
ID	FUT4_MOUSE	STANDARD;	PRT;	433 AA.		
AC	Q11127;					
DT	01-OCT-1996 (Rel. 34, Created)					
DT	01-OCT-1996 (Rel. 34, Last sequence update)					
DT	01-MAR-2002 (Rel. 41, Last annotation update)					
DE	Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 4) (FUCT-IV).					
GN	FUT4 OR ELFT.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=96027607; PubMed=7559635;					
RA	Gersten K.M., Natsuka S., Trinchera M., Petryniak B., Kelly R.J., Hiraiwa N., Jenkins N.A., Gilbert D.J., Copeland N.G., Lowe J.B.;					
RA	"Molecular cloning, expression, chromosomal assignment, and tissue-specific expression of a murine alpha-(1,3)-fucosyltransferase locus corresponding to the human ELAM-1 ligand fucosyl transferase.";					
RL	J. Biol. Chem. 270:25047-25056(1995).					
RN	[2]					
RP	SEQUENCE FROM N.A. (SHORT FORM).					
RC	STRAN-129/SV; TISSUE=Liver;					
RX	MEDLINE=97037075; PubMed=8882722;					
RA	Ozawa M., Muramatsu T.;					
RT	"Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene that shows homology with the human alpha-1,3 fucosyltransferase IV gene.";					
RL	J. Biochem. 119:302-308(1996).					
CC	-1- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.					
CC	-1- PATHWAY: GLYCOSYLATION.					
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.					
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.					
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN STOMACH AND COLON. IT ALSO EXPRESSED IN THE LUNG, TESTIS, UTERUS, SMALL INTESTINE AND TO A LESSER EXTENT IN SPLEEN, AND OVARY. PRESENT IN TRACE AMOUNTS IN BRAIN, THYMUS, HEART, SMOOTH MUSCLE, KIDNEY AND BONE MARROW. NOT FOUND IN LIVER, SALIVARY GLAND AND PANCREAS.					
CC	-1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.					
CC	-----					
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CC	-----					
DR	EMBL; U33457; AAC52269.1; -;					
DR	EMBL; D63380; BAA09697.1; -;					

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DR EMBL; D63379; BAA09696.1; --
DR MGI; 95594; Fut4.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Gold; 52
FT DOMAIN 1 52
FT TRANSMEM 53 74
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT POTENTIAL.
FT DOMAIN 75 433
FT CARBOHYD 117 117
FT CARBOHYD 218 218
FT VARSPLIC 1 33
FT CONFLICT 252 252
FT CONFLICT 257 257
FT CONFLICT 260 260
FT CONFLICT 273 273
SQ SEQUENCE 433 AA; 49481 MW; 2401822F02B5D021 CRC64;

Query Match 35.8%; Score 706; DB 1; Length 433;
Best Local Similarity 42.7%; Pred. No. 2.6e-45;
Matches 146; Conservative 48; Mismatches 96; Indels 52; Gaps 8;

QY 66 TLVWVWPF---GQTFDLTSCQAMENIQGCHLTDRSLYNKSHAVLIHHRDISWDLTNP 121
DB 92 VLLWEPFRGRGGYKSPDCLSFENISGCLLTDRAYGEAQVLEHHRDIVKELHWP 151
QY 122 QY---
DB 152 PPWAGRETDKALVLRVFDQEGAVTGTGALETGVGRPPQQRWNNFSPSHTPGLRG 211
QY 148 I-EHLNLTLYRSDSDIQVPGFLTVSTNPFVFEVPS-----KEKLVCVWVSNWNP 198
DB 212 LAKDLFNWTLSTYRSDSDIVFVPGFLYPRSDP--TEQPSGLGPOLARKRGLVAVVYVSHW 269
QY 199 EHARVYKYNELSKSIEHTYQAF-GEYVNDKNLIPTISTCKFYLSFENSIIHKDYITEKL 257
DB 270 HQARVRYTHQLRRHVSVDVFGRTGPRVPAIGLLHTVARYKFLAFENSQHVVDYITEKL 329
QY 258 Y-NAFLAGSVVPLGSPRENYENIPADSFTHVEDNSPSELAKYLKVDKNKKNLYLSYF 316
DB 330 WRNAPLAGAVPVLGPDPRANYERVPVPGAFTHVDVDFNPAASLAAYLLFLDRNAVYRYF 389
QY 317 NWKDKFTVNLPRFWSHACLDHVKRH-OEYKSVGNLEKWF 357
DB 390 WRRSFVAHIITSFWEDEQWCRCTQAVQTSQDQPKSIHNLADWF 431

RESULT 2
FUT4_RAT
AC Q62994; STANDARD; PRT; 433 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1.3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-
DE fucosyltransferase) (Fucosyltransferase 4) (FUCT-IV).
GN FUT4 OR RFUC-T.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
EX MEDLINE=97265205; PubMed=911142;
RA Sajdel-Sulkowska E.M., Smith F.L., Wiederschain G., McCluer R.H.;
RT "Cloning of a rat alpha1,3-fucosyltransferase gene: a member of the
RT fucosyltransferase IV family."
RL Glycoconj. J. 14:249-258(1997).
CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SEA-1 AND VIM-2 ANTIGENS.
CC -1- PATHWAY: GLYCOSYLATION.

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CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN ADULT, HIGHEST EXPRESSION IN SPLEEN,
CC TESTIS, BRAIN, LUNG, KIDNEY AND SKELETAL MUSCLE AND TO A LESSER
CC EXTENT IN LIVER AND HEART.
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
CC
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CC
CC EMBL; U58860; AAB97609.1; --
CC InterPro: IPR001503; Glyco_transf_10.
CC Pfam; PF00852; Glyco_transf_10; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Gold; 52
FT DOMAIN 1 54
FT TRANSMEM 55 74
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT POTENTIAL.
FT DOMAIN 75 433
FT CARBOHYD 117 117
FT CARBOHYD 218 218
FT VARSPLIC 1 33
FT SEQUENCE 433 AA; 48779 MW; 75B0E569B72FD2F8 CRC64;

Query Match 35.3%; Score 694.5; DB 1; Length 433;
Best Local Similarity 39.1%; Pred. No. 1.9e-44;
Matches 158; Conservative 52; Mismatches 119; Indels 75; Gaps 13;

QY 4 TSKGLRLRPLIVCIILGCFMACLLIYIKPTNSWVSPESASVLYKMKNFSTKTDYFNE 63
DB 53 TSSGLAAGLL-CTAL---TACLCWGQLPLPWA-SPAQ-----RP 89
QY 64 TTLVWVWPF---GQTFDLTSCQAMENIQGCHLTDRSLYNKSHAVLIHHRDI----- 113
DB 90 VSVLLWEPFRGRGGHSPDCLSFENISGCLLTDRAYGEAQVLEHHRDIVKELHWP 149
QY 114 ---SWDLTNLPQA-----RPPQKWTWNLESPTHTPQK 145
DB 150 WPPWGAQERTDEALELRVFDQEGAVMLAREALTTGSRPPGQWVMMNFSPSHTPGL 209
QY 146 SGI-EHLNLTLYRSDSDIQVPGFLTVSTNPFVFEVPS-----KEKLVCVWVSNW 196
DB 210 RGLAKDLFNWTLSTYRSDSDIVFVPGFLYPRSHP--AEQPSGLGPPLARKRGLVAVVYSHW 267
QY 197 NPEHARVYKYNELSKSIEHTYQAF-GEYVNDKNLIPTISTCKFYLSFENSIIHKDYITE 255
DB 268 NERQARVRYTHQLRRHVSVDVFGRTGPRVPAIGLLHTVARYKFLAFENSQHVVDYITE 327
QY 256 KLY-NAFLAGSVVPLGSPRENYENIPADSFTHVEDNSPSELAKYLKVDKNKKNLYLS 314
DB 328 KLWRNAPLAGAVPVLGPDPRANYERVPVPGAFTHVDVDFNPAASLAAYLLFLDRNAVYRY 387
QY 315 YFNWRKDTVNLPRFWSHACLDHVKRH-OEYKSVGNLEKWF 357
DB 388 YFHWRSYAVHIITSFWEDEQWCRCTQAVQTSQDQPKSIHNLADWF 431

RESULT 3
FUT4_HUMAN
ID FUT4_HUMAN STANDARD; PRT; 405 AA.
AC P22083;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1.3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-
DE fucosyltransferase) (Fucosyltransferase 4) (FUCT-IV) (ELAM-1 ligand

```

DE fucosyltransferase).

GN FUT4 OR LEFT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood leukocytes;

RX MEDLINE=91373370; PubMed=1716630;

RA Lowe J.B., Kukowska-Latallo J.F., Nair R.P., Larsen R.D., Marks R.M.,

RA Macher B.A., Kelly R.J., Ernst L.K.;

RT "Molecular cloning of a human fucosyltransferase gene that determines

RT expression of the Lewis x and VIM-2 epitopes but not ELAM-1-dependent

RT cell adhesion.";

RL J. Biol. Chem. 266:17467-17477(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91084863; PubMed=1702034;

RA Goelz S.E., Hession C., Goff D., Griffiths B., Tizard R., Newman B.,

RA Chi-Rosso G., Lobb R.;

RT "ELF1: a gene that directs the expression of an ELAM-1 ligand.";

RL Cell 63:1349-1356(1990).

RN [3]

RP SEQUENCE OF 1-400 FROM N.A.

RX MEDLINE=92042084; PubMed=1718983;

RA Kumar R., Potvin B., Muller W.A., Stanley P.;

RT "Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes

RT ELF1 but does not confer ELAM-1 recognition on Chinese hamster ovary

RT cell transfectants.";

RL J. Biol. Chem. 266:21777-21783(1991).

CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN

CC THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.

CC -!- PATHWAY: GLYCOSYLATION.

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

CC FORM IN TRANS CISTERNAE OF GOLGI.

CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

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CC or send an email to license@isb-sib.ch).

DR EMBL; M65030; AAA92977.1; -

DR EMBL; M58596; AAA63172.1; -

DR EMBL; M58597; AAA63173.1; ALT_INIT.

DR EMBL; S65161; AAB20349.1; -

DR PIR; A36340; A36340.

DR MIM; 104230; -

DR InterPro; IPR001503; Glyco_transf_10.

DR Pfam; PF00852; Glyco_transf_10; 1.

KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;

KW Signal-anchor; Golgi stack.

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 23 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT POTENTIAL).

FT DOMAIN 48 405 LUMENAL, CATALYTIC (POTENTIAL).

FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 87 87 P -> R (IN REF. 2 AND 3).

FT CONFLICT 241 241 E -> D (IN REF. 3).

SQ SEQUENCE 405 AA; 45569 MW; DE72ELFDC390268D CRC64;

Query Match 35.1%; Score 691.5; DB 1; Length 405;

Best Local Similarity 38.8%; Pred. No. 2.9e-44;

Matches 154; Conservative 58; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI-----KPTNSWVSPMESASSVLKMKNFSTKTDYFNETTILV 68

DB 28 VCVLAAGLTCTALITYACWGQLPPLPWA-SPTPS-----RPGVLL 68

QY 69 WYWPFGQTDL-----TSCQAMFNIQCHLTDRSLYNKSHAVLIHRI-----SW----- 115

DB 69 WWPFGGSDSAPRPPDCPLRFNISGRLLTDRASYGEAQAVLFHRLDLVKGPPDPWP 128

QY 116 -----DLTNLPQ-----ARPPQKWIWMNLESPTHTP-QKSGIEHL 151

DB 129 GQAHFAEVDLRLVDEEAAAAAALATSSPPGQQRWWMNFESFSGSLASNL 188

QY 152 FNULTYRRSDIQVPYGLTVSTNPFVFPVS-----KEKLYCVVSNMNPHEARY 203

DB 189 FNNWTLSTRADSDVFPVGYLPRSHP--GDPPSGLAPLSRKQGLVAVVYSHWDERQARV 246

QY 204 KYNELSKSIEIHTYQAP-GEYVNDKNLIPTISTCKFYLSPFNSHDKYHTEKLY-NAF 261

DB 247 RYHQLSQHVTVDVFGGPGQVPEIGLHTVARYKFKYLAFFENSOHLDTITEKLARNAL 306

QY 262 LAGSVPVVLGSPRENYENIPADSFTHVEDFNSPSELAKYLKEVDKNNKLYLYSEYENWRKD 321

DB 307 LAGAVPVVLGPDPRANRYERFVRGAFIHVDFFPSASSLASLYLLFLDRNPVRYRYFHWRSS 366

QY 322 FTVNLPFRFWSHACLACDHVKRHOEY-KSYGNLEKWF 357

DB 367 YAVHITSFWDEPWCRCVQAVQVRAGDRPKSIRNLASWF 403

RESULT 4

ID FUT3_HUMAN STANDARD; PRT; 361 AA.

AC P21217; Q99448; Q99449;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis

DE alpha-4-fucosyltransferase) (Lewis Ft) (Fucosyltransferase 3) (FUCT-

DE III).

GN FUT3 OR LE OR FT3B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91032981; PubMed=1977660;

RA Kukowska-Latallo J.F., Larsen R.D., Nair R.P., Lowe J.B.;

RT "A cloned human cDNA determines expression of a mouse stage-specific

RT embryonic antigen and the Lewis blood group

RL alpha(1,3/1,4)-fucosyltransferase.";

RL Genes Dev. 4:1288-1303(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95378269; PubMed=7650030;

RC TISSUE=Liver;

RX Cameron H.S., Szczepaniak D., Weston W.;

RA "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase

RT genes in normal tissues. Alternative splicing, polyadenylation, and

RT isoforms.";

RL J. Biol. Chem. 270:20112-20122(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Squamous cell carcinoma;

RA Rahm I., Schmidt L.R., Wahl D., Drayson E., Maslanik W.,

RA Stranahan P.L., Pettijohn D.E.;

RT "Isolation and expression of human alpha (1,3/1,4)

RT fucosyltransferase.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP VARIANT LE(-) MET-105.

RX MEDLINE=94059067; PubMed=8240322;

RA Elmgren A., Rydberg L., Larson G.;

RT "Genotypic heterogeneity among Lewis negative individuals.";

RL Biochem. Biophys. Res. Commun. 196:515-520(1993).

RN [5]

RP VARIANTS LE(-) ARG-20; SER-170 AND ALA-336.
 RX MEDLINE=94059082; PubMed=8240337;
 RA Nishihara S., Yazawa S., Iwasaki H., Nakazato M., Kudo T., Ando T.,
 RA Narimatsu H.;
 RT "Alpha (1,3/1,4)fucosyltransferase (FucT-III) gene is inactivated by
 RT a single amino acid substitution in Lewis histo-blood type negative
 RT individuals.";
 RL Biochem. Biophys. Res. Commun. 196:624-631(1993).
 RN [6]
 RP VARIANTS LE(-) ARG-20 AND SER-170.
 RX MEDLINE=94033579; PubMed=8219240;
 RA Koda Y., Kimura H., Mekada E.;
 RT "Analysis of Lewis fucosyltransferase genes from the human gastric
 RT mucosa of Lewis-positive and -negative individuals.";
 RL Blood 82:2915-2919(1993).
 RN [7]
 RP VARIANTS LE(-) ARG-20 AND LYS-356.
 RX MEDLINE=94342259; PubMed=8063716;
 RA Mollicone R., Reguigne I., Kelly R.J., Fletcher A., Watt J., Oriol R.;
 RA Chatfield S., Aziz A., Cameron H.S., Weston B.W., Lowe J.B., Oriol R.;
 RT "Molecular basis for Lewis alpha(1,3/1,4)-fucosyltransferase gene
 RT deficiency (FUT3) found in Lewis-negative Indonesian pedigrees.";
 RL J. Biol. Chem. 269:20987-20994(1994).
 RN [8]
 RP VARIANTS LE(-) LYS-356.
 RX MEDLINE=95050753; PubMed=7961897;
 RA Nishihara S., Narimatsu H., Iwasaki H., Yazawa S., Akamatsu S.,
 RA Ando T., Seno T., Narimatsu I.;
 RT "Molecular genetic analysis of the human Lewis histo-blood group
 RT system.";
 RL J. Biol. Chem. 269:29271-29278(1994).
 RN [9]
 RP VARIANTS LE(-) ARG-20; ARG-68; MET-105 AND LYS-356.
 RX MEDLINE=96243526; PubMed=8801770;
 RA Elmgren A., Boerjeson C., Svensson L., Rydberg L., Larson G.;
 RT "DNA sequencing and screening for point mutations in the human Lewis
 RT 'FUT3' gene enables molecular genotyping of the human Lewis blood
 RT group system.";
 RL Vox Sang. 70:97-103(1996).
 RN [10]
 RP VARIANTS LE(-) ARG-68 AND MET-105.
 RX MEDLINE=97413801; PubMed=9268337;
 RA Elmgren A., Mollicone R., Costache M., Boerjeson C., Oriol R.,
 RA Harrington J., Larson G.;
 RT "Significance of individual point mutations, T202C and C314T, in the
 RT human Lewis 'FUT3' gene for expression of Lewis antigens by the human
 RT alpha'1,3/1,4'-fucosyltransferase, Fuc-TIII.";
 RL J. Biol. Chem. 272:21994-21998(1997).
 RN [11]
 RP VARIANTS LE(+) K-102 AND A-124, AND VARIANTS LE(-) N-162; R-223 AND
 RP M-270.
 RX MEDLINE=98366989; PubMed=9703429;
 RA Pang H., Liu Y., Koda Y., Soejima M., Jia J., Schlaphoff T.,
 RA du Toit E.D., Kimura H.;
 RT "Five novel missense mutations of the Lewis gene 'FUT3' in African
 RT 'Xhosa' and Caucasian populations in South Africa.";
 RL Hum. Genet. 102:675-680(1998).
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
 CC INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS A, LEWIS B, STALYL
 CC LEWIS X AND LEWIS X/SSA-1 ANTIGENS, MAY BE INVOLVED IN BLOOD
 CC GROUP LEWIS DETERMINATION; LEWIS-POSITIVE (LE(+)) INDIVIDUALS
 CC HAVE AN ACTIVE ENZYME WHILE LEWIS-NEGATIVE (LE(-)) INDIVIDUALS
 CC HAVE AN INACTIVE ENZYME.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 CC N-ACETYL-D-GLUCOSAMINYL-R = GDP + 1,3-BETA-D-GALACTOSYL-
 CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYL-R.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN STOMACH, COLON, SMALL
 CC INTESTINE, LUNG AND KIDNEY AND TO A LESSER EXTENT IN SALIVARY
 CC GLAND, BLADDER, UTERUS AND LIVER.
 CC -1- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL

CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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 CC -----
 CC EMBL: X53578; CAA37641.1; -
 DR EMBL: U27328; AAC50187.1; -
 DR EMBL: U27326; AAC50185.1; -
 DR EMBL: U27327; AAC50186.1; -
 DR EMBL: D89324; BAA13941.1; -
 DR EMBL: D89325; BAA13942.1; -
 DR EMBL: AF131913; AAD33514.1; -
 DR PIR: A36669; A36669.
 DR MIM: 111100; -
 DR InterPro: IPR001503; Glyco_transf_10.
 DR Pfam: PF00852; Glyco_transf_10; 1.
 DR Transfaser: Glycosyltransferase; Glycoprotein; Transmembrane;
 KW Signal-anchor; Golgi stack; Polymorphism; Blood group antigen.
 FT DOMAIN 1 15
 FT TRANSMEM 16 34
 FT DOMAIN 35 361
 FT CARBOHYD 154 154
 FT CARBOHYD 185 185
 FT VARIANT 20 20
 FT VARIANT 68 68
 FT VARIANT 102 102
 FT VARIANT 105 105
 FT VARIANT 124 124
 FT VARIANT 162 162
 FT VARIANT 170 170
 FT VARIANT 223 223
 FT VARIANT 270 270
 FT VARIANT 336 336
 FT VARIANT 356 356
 FT SEQUENCE 361 AA; 42117 MW; BF4398044F19C284 CRC64;
 FT Query Match 34.08; Score 670; DB 1; Length 361;
 FT Best Local Similarity 43.48; Pred. No. 9.9e-43;
 FT Matches 132; Conservative 54; Mismatches 98; Indels 20; Gaps 9;
 QY 66 ILVWVWPGQFDLTSCQMF-NIQGCHLTDRSLYKSHAVLIHHRDISWDL-----TN 119
 DB 65 ILTWTPQGHIPVALSRCEMVGPTADCHITADRKVYQADTVIVHH---WDIMNSPKSR 120
 QY 120 LPQARPPQFKWIMWNLESPTHTPKSGIEHLNLTLYRDSDIQVPGFLTV-STNPF 178
 DB 121 LPPSPRQGRWIFNLEPPNPPNQHLALDRYFNLTSYRSDSDIFTYPGWLEPWSGQA 180
 QY 179 --VFEPVSKERKLVGVVSNWNPENHARVYKYNELSKSIEHTYQAFGYVNDKMLIPTIS 236
 DB 181 HPPLNLSAKTELVAWVSNWKPDSARVRYQSLQHLKVDVYGRSH-KPLPKGTMMETLS 239
 QY 237 TCKFYLSFENSITKDYITEKLY-NAFLAGSVPVVLGSPRSRENYENIPADSFHVEDENSP 295
 DB 240 RYKFLAFENSLHPDYITEKLRNALNALEAWVPVVLGSPRSRNYERFLPPDAFIHVDQSP 299


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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X87810; CAA61079.1;
CC InterPro; IPR001503; Glyco_transf_10.
CC Pfam; PF00852; Glyco_transf_10; 1.
CC Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Signal-anchor; Golgi stack.
CC DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
CC TRANSFEM 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 35 365 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (PROBABLE).
CC FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (PROBABLE).
CC FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (PROBABLE).
CC SEQUENCE 365 AA; 42654 MW; 18715A361B0025D3 CRC64;
CC -----
Query Match 34.0%; Score 669; DB 1; Length 365;
Best Local Similarity 39.4%; Pred. No. 1.2e-42;
Matches 145; Conservative 66; Mismatches 115; Indels 42; Gaps 12;
QY 11 PELIVCIILG-CFMACLLI---YIKPTNSW-----FSPMESASSVLKMKNFSTKTDY 60
DB 18 PGLLLQLLALCFSSYLRMSQKPKPKPMVMSLGPASQATGSSAHLPLR----- 68
QY 61 FNETTIVWVPFGQTFDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISW-DLT 118
DB 69 -----VLLTWPFNTFVALSRCSLWPGTADCOLTVNRSEYPOQADAVLVHREVSHPOM 123
QY 119 NLPOQARPPFOKWIWNLESPTHTPKSGIEHLFNLTLTYRRSDSDIOPVYCYFL-----T 172
DB 124 QLPPSPRPQGWVWFMSFSPNSCLKLDLGYFNLTWSYRRSDSDIFWPYGNLEPWPSP 183
QY 173 VSTNPFVEVPSEKELVGVVSNWNPENHARVYKYNLSKSIETHTYQAGFYVNDKNLI 232
DB 184 VET---LLNISAKTLVAVVSNWNTDSIRVOYKLLKPHLOVDVYGR-FHTPLPALMA 239
QY 233 PTISCKEYLPSPENSHKDYITEKLY-NAFLAGSVPVVLGSPRENYENIADSFHVED 291
DB 240 KOLSQYKYLAFENSLHPDYITEKLRNALQAWVAVVGLGFSRVNYEQFLPKAFIHVED 299
QY 292 FNSPSELAKYLEVDKNNKLYLYSNFNRKDFTVNLP--FWESHACIACDHVKRHOEYKS 349
DB 300 FOSPDLAQYLLALDKDYASYLYNYPFRWETLR---PRSFWMALPCKACWKLOQEPRYQT 356
QY 350 VGNLEKWF 357
DB 357 VPSIASWF 364
RESULT 7
FUT5_PANTR
ID FUT5_PANTR STANDARD; PRT; 374 AA.
AC P56433;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1.3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-
DE fucosyltransferase) (Fucosyltransferase 5) (FUCT-V).
GN FUT5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_Taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98037800; PubMed=9368041;

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RA Costache M., Apoil P.-A., Calileau A., Elmgren A., Larson G.,
RA Henry S., Blanchard A., Iordachescu D., Oriol R., Mollicone R.;
RA "Evolution of fucosyltransferase genes in vertebrates.";
RL J. Biol. Chem. 272:29721-29728(1997).
CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF VIM-2, LEWIS X/SSEA-1 AND SIALYL LEWIS X
CC ANTIGENS (BY SIMILARITY).
CC CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
CC N-ACETYL-D-GLUCOSAMINYLR-R = GDP + 1,3-BETA-D-GALACTOSYL-
CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR-R.
CC -1- PATHWAY: GLYCOSYLATION
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CISTERNAE OF GOLGI.
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y14034; CAA74361.1;
CC InterPro; IPR001503; Glyco_transf_10.
CC Pfam; PF00852; Glyco_transf_10; 1.
CC Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
CC Signal-anchor; Golgi stack.
CC DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
CC TRANSFEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 35 374 LUMENAL, CATALYTIC (POTENTIAL).
CC FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 374 AA; 43034 MW; 3F35DEE8A8F1A2E2 CRC64;
CC -----
Query Match 34.0%; Score 669; DB 1; Length 374;
Best Local Similarity 43.3%; Pred. No. 1.2e-42;
Matches 130; Conservative 58; Mismatches 100; Indels 12; Gaps 7;
QY 66 ILVWVWPFQTFDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISW-DLTNLPQQ 123
DB 78 ILLTWPFNTFVALPRCSSEMPVGAACNITADSNVYPOQADAVIVHWDIMYNPSANLPPP 137
QY 124 ARPPQKWIWNLESPTHTPKSGIEHLFNLTLTYRRSDSDIOPVYGYFLTVSTNFV---F 180
DB 138 TRPQGORWIFSMESPSNCRHLEADGYFNLTMSYRRSDSDIFTYPGLQPMWSPGVHPPL 197
QY 181 EVPSKEKLVGVVSNWNPENHARVYKYNLSKSIETHTYQAGFYVNDKNLIPTISCKF 240
DB 198 NLSAKTELVAWVSNWGNPNSARVRYQSLOAHLKVDVYGRSH-KPLPQGTMMETLSRYKF 256
QY 241 YLSPENSILKDYITEKLY-NAFLAGSVPVVLGSPRENYENIADSFTHVEDNSPSELA 299
DB 257 YLAFENSLHPDYITEKLRNALQAWVAVVGLGFSRVNYERFLPPDAFTHVDDFQSPKDLA 316
QY 300 KYLEVDKNNKLYLYSNFNRKDFTVNLP--FWESHACIACDHVKRHOEYKSVGNLEKWF 357
DB 317 RYQLQELDKHARYLYSYFWRWETLR---PRSFWMALPCKACWKLOQPSRYQTVSIAAWF 373
RESULT 8
FUT6_HUMAN
ID FUT6_HUMAN STANDARD; PRT; 359 AA.
AC P51993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-(1.3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-
DE fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).
GN FUT6 OR FCT3A.

```


OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92392318; PubMed=1520296;
 RA Koszidin K.L., Bowen B.R.;
 RT "The cloning and expression of a human alpha-1,3 fucosyltransferase
 RT capable of forming the E-selectin ligand.";
 RL Biochem. Biophys. Res. Commun. 187:152-157(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=93077550; PubMed=1339443;
 RA Weston B.W., Smith P.L., Kelly R.J., Lowe J.B.;
 RT "Molecular cloning of a fourth member of a human alpha
 RT (1,3)fucosyltransferase gene family. Multiple homologous sequences
 RT that determine expression of the Lewis x, sialyl Lewis x, and
 RT difucosyl sialyl Lewis x epitopes.";
 RL J. Biol. Chem. 267:24575-24584(1992).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RC MEDLINE=95378269; PubMed=7650030;
 RA Cameron H.S., Szczepaniak D., Weston B.W.;
 RT "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
 RT genes in normal tissues. Alternative splicing, polyadenylation, and
 RT isoforms.";
 RL J. Biol. Chem. 270:20112-20122(1995).
 CC -1- FUNCTION: ENZYME INVOLVED IN THE BIOSYNTHESIS OF THE E-SELECTIN
 CC LIGAND. SIALYL-LEWIS X CATALYZES THE TRANSFER OF FUCOSE FROM GDP-
 CC BETA-FUCOSE TO ALPHA-2,3 SIALYLATED SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR =
 CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER, COLON, SMALL INTESTINE,
 CC BLADDER, UTERUS AND SALIVARY GLAND.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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 CC -----
 DR EMBL; M98825; AAA9222.1; -
 DR EMBL; L01698; AAB03078.1; -
 DR EMBL; U27333; AAC50192.1; -
 DR EMBL; U27334; AAC50193.1; -
 DR EMBL; U27335; AAC50194.1; -
 DR EMBL; U27336; AAC50195.1; -
 DR EMBL; U27331; AAC50190.1; -
 DR EMBL; U27332; AAC50191.1; ALT_SEQ.
 DR EMBL; U27337; AAC50196.1; -
 DR MIM; 136836; -
 DR InterPro; iPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
 KW Signal-anchor; Golgi stack; Alternative splicing.
 FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
 FT TRANSFERRASE 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 35 359 LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT

FT VARSPLIC 348 359 RVQTRGIAAWFT -> SSGGLIYLRTRLPEASPA (IN
 FT SEQUENCE 359 AA; 41859 MW; 67ABDF058F0999DA CRC64;
 SQ
 Query Match 33.8%; Score 665.5; DB 1; Length 359;
 Best Local Similarity 43.1%; Pred. No 2.1e-42;
 Matches 134; Conservative 58; Mismatches 106; Indels 13; Gaps 9;
 QY 55 STKTDYFNETTILVWVWPFQGTEDLTSCQAMF-NIOGCHLTTRDSLYNKSHAVLIHHRDI 113
 DB 53 STGTPAHSIPLILLWTWPNKPIALPCRSBMPGTADCNITADRKVYPQADAVIVHREV 112
 QY 114 SWD-LTNLQQARPPFQKWIWNWLNLESTHTPQSGTEHLENLTLYRRDSDIOVPGFLT 172
 DB 113 MYNPSAQLPRSPRQGRQWIFSMESPSHCWQLKAMDGVNLTMSYRSDSDIFTPYGWLE 172
 QY 173 V-STNPF--VFVEPSKEKLVCCWVSNWNPCHARKVYNNLSKSIETHTYQOAFGEVYNDK 229
 DB 173 PWSGQPAHPPLNLSAKTELVAWAVSNWGNPSARVYQSLQAHLKVDVYGRSH-KPLPQG 231
 QY 230 NLTIPTSTCKFYLSFENSITKDYITEKLY-NAFLAGSVVVLGSPRSRENYENIPADSFTI 288
 DB 232 TMMETLSRYKFKYLAENSLHPDYITEKLRNALAEAWAVPVVLGSPRSNRYERFLPPDAFIH 291
 QY 289 VEDFNSPSELAKYLKEVDKNNKLYLSFYFNWRKDFTYNLP--FWESHACIACDHYKRRQE 346
 DB 292 VDDFQSPKDIARYLQELDKDHARYLSYFRWRETLR---PRFSWALAFKACWKLOEBSR 348
 QY 347 YKSVGNLEKWF 357
 DB 349 YQTRG-IAAWF 358
 RESULT 9
 ID FUT3_PANTR STANDARD; PRT; 372 AA.
 AC Q19058;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis
 DE alpha-4-fucosyltransferase) (Lewis Ft) (Fucosyltransferase 3) (FUCT-
 DE III) (Alpha-3/4-fucosyltransferase).
 GN FUT3.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98037800; PubMed=9368041;
 RA Costache M., Apoil P.-A., Caillieu A., Elmgren A., Larson G.,
 RA Henry S., Blancher A., Iordachescu D., Oriol R., Mollicone R.;
 RT "Evolution of fucosyltransferase genes in vertebrates.";
 RL J. Biol. Chem. 272:29721-29728(1997).
 CC -1- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES
 CC INVOLVED IN THE EXPRESSION OF SIALYL LEWIS X AND LEWIS X/SSSEA-1
 CC ANTIGENS. IT MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 CC N-ACETYL-D-GLUCOSAMINYLR = GDP + 1,3-BETA-D-GALACTOSYL-
 CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR.
 CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES (A AND B). ALLELE A HAS ARG-
 CC 162 AND VAL-304. ALLELE B HAS GLY-162 AND MET-304.
 CC -1- MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL
 CC DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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CC EMBL; Y14033; CAA74360.1; -
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
 KW Signal-anchor; Golgi stack; Polymorphism.
 FT DOMAIN 1 14 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT TRANSMEM 15 34 (POTENTIAL).
 FT DOMAIN 35 372 LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 162 162 R -> G (IN ALLELE B).
 FT VARIANT 304 304 V -> M (IN ALLELE B).
 FT SEQUENCE 372 AA; 43233 MW; 649CBFB8CA/BD74C CRC64;

Query Match 33.7%; Score 663; DB 1; Length 372;
 Best Local Similarity 43.7%; Pred. No. 3.4e-42;
 Matches 131; Conservative 56; Mismatches 101; Indels 12; Gaps 8;
 QY 66 ILVWVWPGQTFDITSCQAMP-NIQGCHLTDRSLYKNSHAVLIHHRDISWD-LTNLPQQ 123
 DB 76 ILLTWPFPHIPVALSRGSEMVPGAACHITADRVYVQADAVIHWIDIMYNPKSLRPPS 135
 QY 124 ARPFPQKWMNLESPTHTPOKSGIEHLNLTLYRRDSDIQVYGFGLTV-STNPF--VF 180
 DB 136 PRPQGRQWIFNLEPPPPNCHLEALDRYFNLTMSYRSDSDIFTYPYGLWLEPWSGPAHPPL 195
 QY 181 EVPSEKLVWVSNWNPENHARVYKYNELSKSTIEHTYGOAFGEYVNDKNLIFTISTCKF 240
 DB 196 NLSAKTELAVAVSNWKLDSARVRYQSLQAHLKVDVYGRSH-KPLPKGTMMETLSRYKF 254
 QY 241 YLSPENSTHKDYITEKLY-NAFLAGSVVVLGSPRENYKYPADSFIVHEDFNSSELA 299
 DB 255 YLAFENSLHPDYITEKLWRNALEAWVPVVLGSPRSNYERFLPDAFIHVDQSPADLA 314
 QY 300 KYLEVDKNNKLYLSYNWRKDFVNLPR--FWESHACLADHVKHQYKSVGNLEKWF 357
 DB 315 RYLOELDKHARYLSYFWRRETLR---PRFSWALDFCKACWKLOQESRYQYMRSTAAMF 371

RESULT 10
 FUT6_PANTR STANDARD; PRT; 359 AA.
 AC P56434;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-
 fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).
 GN FUT6.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata.
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98037800; PubMed=9368041;
 RA Costache M.; Apoll P.-A.; Calileau A.; Elmgren A.; Larson G.;
 RA Henry S.; Blancher A.; Iordachescu D.; Oriol R.; Mollicone R.;
 RT Evolution of fucosyltransferase genes in vertebrates.
 RL J. Biol. Chem. 272:29721-29728(1997).
 CC -1- FUNCTION: ENZYME INVOLVED IN THE BIOSYNTHESIS OF THE E-SELECTIN
 CC LIGAND, SIALYL-LEWIS X. CATALYZES THE TRANSFER OF FUCOSE FROM GDP-
 CC BETA-FUCOSE TO ALPHA-2,3 SIALYLATED SUBSTRATES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: GDP-L-FUCOSE + 1,3-BETA-D-GALACTOSYL-
 CC N-ACETYL-D-GLUCOSAMINYLR = GDP + 1,3-BETA-D-GALACTOSYL-
 CC (ALPHA-1,4-L-FUCOSYL)-N-ACETYL-D-GLUCOSAMINYLR.

CC -1- PATHWAY: GLYCOSYLATION.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES, A AND B. ALLELE A HAS PRO-
 CC 124, GLN-172 AND VAL-192. ALLELE B HAS LEU-124, GLU-172 AND ALA-
 CC 192.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
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CC EMBL; Y14035; CAA74362.1; -
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
 KW Signal-anchor; Golgi stack; Polymorphism.
 FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 35 359 LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 124 124 P -> L (IN ALLELE B).
 FT VARIANT 172 172 Q -> E (IN ALLELE B).
 FT VARIANT 192 192 V -> A (IN ALLELE B).
 FT SEQUENCE 359 AA; 41892 MW; 207C3DC29B2BFD3 CRC64;

Query Match 33.6%; Score 662.5; DB 1; Length 359;
 Best Local Similarity 42.1%; Pred. No. 3.5e-42;
 Matches 131; Conservative 61; Mismatches 106; Indels 13; Gaps 8;
 QY 55 SKTDYFNETTILVWVWPGQTFDITSCQAMP-NIQGCHLTDRSLYKNSHAVLIHHRDI 113
 DB 53 SYGTFAHSIPLILLTWPFPHIPVALSRGSEMVPGAACHITADRVYVQADAVIHWIDIMYNPKSLRPPS 112
 QY 114 SWD-LTNLPQARPPQKWMNLESPTHTPOKSGIEHLNLTLYRRDSDIQVYGFGLT 172
 DB 113 MYNPSAQLPRSPRQGRQWIFNFSMESPCNCRHLEALDGYFNLTMSYRSDSDIFTYPYGLW 172
 QY 173 VSTNPFV---FEVPSKEKLVWVSNWNPENHARVYKYNELSKSTIEHTYGOAFGEYVNDK 229
 DB 173 PWSGQPVHPPLNLSAKTELAVAVSNWGNPNSARVRYQSLQAHLKVDVYGRSH-KPLPQ 231
 QY 230 NLIPTISTCKFYLSFENSTHKDYITEKLY-NAFLAGSVVVLGSPRENYKYPADSFIVH 288
 DB 232 TMWETLSRYKFLAFENSLHPDYITEKLWRNALEAWVPVVLGSPRSNYERFLPDAFIH 291
 QY 289 VEDFNSPSELAKYLEVDKNNKLYLSYNWRKDFVNLPR--FWESHACLADHVKHQYK 346
 DB 292 VDDFOSPKDLARYLQELDKHARYLSYFWRRETLR---PRFSWALAFCKACWKLOQESR 348
 QY 347 YKSVGNLEKWF 357
 DB 349 YQT-RSIAAWF 358

RESULT 11
 FUT7_HUMAN STANDARD; PRT; 342 AA.
 ID FUT7_HUMAN
 AC Q11130;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-
 fucosyltransferase) (Fucosyltransferase 7) (FUCT-VII) (Selectin-
 DE ligand synthase).
 GN FUT7.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=94266898; PubMed=8207002;
 RX Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.;
 RA "Molecular cloning of a cDNA encoding a novel human leukocyte
 RT alpha-1,3-fucosyltransferase capable of synthesizing the sialyl
 RT Lewis x determinant.";
 RL J. Biol. Chem. 269:16789-16794(1994).
 RN [2]
 RP REVISIONS.
 RX MEDLINE=94337669; PubMed=8051184;
 RA Natsuka S., Gersten K.M., Zenita K., Kannagi R., Lowe J.B.;
 RT "Molecular cloning of a cDNA encoding a novel human leukocyte
 RT alpha-1,3-fucosyltransferase capable of synthesizing the sialyl
 RT Lewis x determinant.";
 RL J. Biol. Chem. 269:20806-20806(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94237894; PubMed=8182079;
 RA Sasaki K., Kurata K., Funayama K., Nagata M., Watanabe E., Ohta S.,
 RA Hanai N., Nishi T.;
 RT "Expression cloning of a novel alpha 1,3-fucosyltransferase that is
 RT involved in biosynthesis of the sialyl Lewis x carbohydrate
 RT determinants in leukocytes.";
 RL J. Biol. Chem. 269:14730-14737(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Hiraawa N., Hiraawa M., Kannagi R.;
 RT "The human selectin-ligand synthase (hFuc-T VII) gene structure and
 RT characterization of the promoter.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 CC THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + ALPHA-2,3-NEU-N-ACETYL-1,4-
 CC BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + ALPHA-2,3-
 CC NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-
 CC N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 CC -!- TISSUE SPECIFICITY: LEUKOCYtic/MYELOID LINEAGE CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X78031; CAA54962.1; -;
 DR EMBL; U11282; AAA20488.1; -;
 DR EMBL; U08112; AAA56869.1; -;
 DR EMBL; AB012668; BAA32819.1; -;
 DR MIM; 602030; -;
 DR InterPro; IPR001503; Glyco_transf_10.
 DR Pfam; PF00852; Glyco_transf_10; 1.
 KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 14
 FT TRANSMEM 15 36 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 81
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 161 162 GP -> A (IN REF. 1; AAA56869).
 FT CONFLICT 304 305 RL -> SV (IN REF. 1; AAA56869).
 SQ SEQUENCE 342 AA; 39238 MW; D31BFF90DD64DFAB CRC64;

Query Match 31.6%; Score 622; DB 1; Length 342;
 Best Local Similarity 43.3%; Pred. No. 3.4e-39;
 Matches 130; Conservative 48; Mismatches 108; Indels 14; Gaps 8;
 QY 65 TILVWVWPF-GQTFDLTS--QAMFNIOGCHLTITDRSLYKSHAVLIHHRDISDLTNP 121
 DB 48 TILVWVWPFDPQPELPSTDC-TRYGIARHLISANRSLASADAVVHFHRELQTRRSHLP 106
 QY 122 QQARPPQKIMWNLESPTTPKSGIEHFLNLTLYRRDSIDQVYPYGFITVSTNPEVFE 181
 DB 107 LAQPRGCPVWVWASMESPSHTHGLSHLGIENWVLSVRRSDIFVPCRLPHWGPSP-P 165
 QY 182 VPSKEKLVCVWVSNWNPENHARVYKYNELSKSIEHTYQGAQGEYVNDKNLIPITSTCKFY 241
 DB 166 LPKSRVAAVWVSNFORQLRARLYQLAPHLRVDFVGRANRPLCASCILVPTVAQYRFY 225
 QY 242 LSPENSHTKDYITEKLY-NAFLAGSVVVLGSPSRENYENIPADSFTHVDFENSPSLAK 300
 DB 226 LSFENSQHRDYITTEKFRNALVAGTVPVVLGPPRATTEAFVPADAFVHVDVFGSARELA 285
 QY 301 YLKEVDKNNKLYSYFNWRKDFVNLPRFWESHACLACD---HVKKRQEKYKSGNLEKWF 357
 DB 286 FL--TGMNESRYQRFPAWRDLRLVFTDWRERCAICDRYPLHPSQVYE---DLEGWF 340
 RESULT 12
 ID FUT7_MOUSE STANDARD; PRT; 389 AA.
 AC Q11131;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (Galactoside 3-L-
 DE fucosyltransferase) (Fucosyltransferase 7) (FUCT-VII).
 GN FUT7
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH;
 RX MEDLINE=96215226; PubMed=8626519;
 RA Smith P.L., Gersten K.M., Petryniak B., Kelly R.J., Rogers C.,
 RA Natsuka Y., Alford J.A. III, Scheidegger E.P., Natsuka S., Lowe J.B.;
 RT "Expression of the alpha(1,3)fucosyltransferase Fuc-TVII in lymphoid
 RT aggregate high endothelial venules correlates with expression of L-
 RT selectin ligands.";
 RL J. Biol. Chem. 271:8250-8259(1996).
 CC -!- FUNCTION: MAY CATALYZE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
 CC THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
 CC -!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + ALPHA-2,3-NEU-N-ACETYL-1,4-
 CC BETA-D-GALACTOSYL-N-ACETYL-D-GLUCOSAMINYL-R = GDP + ALPHA-2,3-
 CC NEU-N-ACETYL-1,4-BETA-D-GALACTOSYL-(ALPHA-1,3-L-FUCOSYL)-
 CC N-ACETYL-D-GLUCOSAMINYL-R.
 CC -!- PATHWAY: GLYCOSYLATION.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
 CC FORM IN TRANS CISTERNAE OF GOLGI.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG AND BONE MARROW AND
 CC TO A MUCH LESSER EXTENT IN SPLEEN, SALIVARY GLAND AND SKELETAL
 CC MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----

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CC -----
DR EMBL: U45980: AAC52484.1; -
DR MGD: U45980: AAC52485.1; -
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW transferase; glycosyltransferase; transmembrane; glycoprotein;
KW Signal-anchor; Golgi stack; Alternative splicing.
FT DOMAIN 1 55
FT SIGNAL-ANCHOR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT TRANSFERASE
FT DOMAIN 56 78
FT LUMENAL, CATALYTIC (POTENTIAL).
FT LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 128 128
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIT 1 51
FT MPTPCPACLTGTHRLFPDQKAPSWESKREATCNSSS
FT PGPWAEPTVQ -> MNCI (IN ISOFORM 2).
SQ SEQUENCE 389 AA: 44494 MW: 118FC6B2378B99C6 CRC64;

Query Match 29.5%; Score 582; DB 1; Length 389;
Best Local Similarity 39.3%; Pred. No. 3.7e-36;
Matches 120; Conservative 8;

QY 65 TILVWVWF-----GQEDLTSCQAMENIOGCHLTTRSLYKNSHAVLIHHRDISWD 116
DB 95 TILVHWFTRNPFLPGDT-----C-TRYGMASCRLSANRLLASADAVFHHRELQTR 148
QY 117 LTNLPQQRPPFKWIMNLESPTHKQSGIEHLNLTITRRSDIQVYGLFVSTN 176
DB 149 QSLPLDQRPQGQWQWASMESPSNTGLHFRGIFNWLVSRRSDIFVYGRLEPLSG 208
QY 177 PFVFEVPSKEKLVCWVSNWNPENHARVYKYNELSKSIEIHTYGOAFGEYVNDKNLPTIS 236
DB 209 F-TGPLPAKSMAMWVSNFQERQORAKLYROLAPHQLQVDVFGRRPLCANCLLPTLA 267
QY 237 TCKYVLSPEHSIKDYITEKLY-NAFLAGSVVVLGFSRENYENIYPADSFIVHEDFNPS 295
DB 268 RYRFYLAPENSOHRDYITEKFWRNALAAAGVPAVGPPRATYEAFFVDFVHVDFFSA 327
QY 296 SELAKYKEVDKNKLYLVFNWPKDFVNLPRFWESHACLAC---DHVRRHGEYKSVGN 352
DB 328 RELAVEL-VSMNESRYRGFFAWDRDLRVRLGLDWRREFCTICARYPLPRSQVYE--D 382
QY 353 LEKWF 357
DB 383 LESWF 387

RESULT 13
FUTA_DROME STANDARD; PRT; 503 AA.
AC Q9VUL9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Core alpha-(1,3)-fucosyltransferase A (EC 2.4.1.-).
GN FUCTA or CG6869.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=Canton-S;
RX MEDLINE=21359431; PubMed=11382750;
RA Fabini G, Fredliger A, Altmann F, Wilson J.B.H.;
RT Identification of core alpha 3-fucosylated glycans and cloning of
FT the requisite fucosyltransferase cDNA from Drosophila melanogaster.;
FT Potential basis of the neuroblast-horseradish peroxidase epitope.;
RL J Biol. Chem. 276:28058-28067(2001).
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;

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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Andrews-Pfannkuch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Bayraktaroglu L., Beasly E.M.,
RA Ballew R.M., Basu P., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Busan M.R., Buck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan P.V., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferreira S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fostler C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin N.L., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mactel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.;
SCIENCE 287:2185-2195(2000).
CC -!- FUNCTION: Catalyzes alpha-1,3 glycosidic linkages.
CC (GLCNAC-beta-1,2-Man-alpha-1,6)-Man-beta-1,4-GlcNAc-beta-1,3-
CC (GLCNAC-beta-1,2-Man-alpha-1,6)-Man-beta-1,4-GlcNAc-beta-1,4-
CC Man-alpha-1,6)-Man-beta-1,4-GlcNAc-beta-1,4-(Fuc-alpha-1,3)-
CC GLCNAC-Asn.
CC -!- PATHWAY: Glycosylation.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound
CC form in trans cisternae of Golgi (By similarity).
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE003532; AAC49657.1; ALT_SEQ.
DR EMBL: AJ302045; CAC41641.1;
DR FlyBase: FBgn0036485; FUCTA.
DR InterPro: IPR001503; Glyco_transf_10.
DR Pfam: PF00852; Glyco_transf_10; 1.
KW transferase; glycosyltransferase; glycoprotein; transmembrane;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 10
FT TRANSFERASE
FT TRANSFERASE
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT LUMENAL, CATALYTIC (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT H -> Y (IN REF. 1).
FT CONFLICT 53

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[illegible]

Db 28 VCVLAAGLCTALITYACWGLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQTFDL-----TSCQAMFNIOGCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115
Db 69 WWPFGGRDSAPRPPDCPLRNFISGCHLLTDRASYGGAQAVLFHRLDLVKGPPDWPWP 128
QY 116 -----DLTNLPQO-----ARPPFORWIMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDLRLVDYEEAAAAAALATSSPPRPGQWVMNFESPSHGLSLASNL 188
QY 152 FNLTLYRRDSIOVPYGLFVSTNPFVEFVS-----KEKLVGVVWVNNWPEHARV 203
Db 189 FNTLSTRADSDFVPGYLYPRSHP--GDPFSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEHTYGOAF-GEYVNDKNLPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
Db 247 RYHQLSQHVTVDVFGRGPGQVPVEIGLLHTVARYKFLAFENSQHLDIYITEKLWRL 306
QY 262 LAGSPVVLGSPRENYENIPADSFTHVEDYNSPSELAKYLKVEDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDPRANYERFVRGAFIHDVDFPSASSLASYLFLDRNPVAVYRRYFHWR 366
QY 322 FTVNLPFRWESHACLADHVHQRQY-KSVGNLEKWF 357
Db 367 YAVHTSFDEWPCWCRVQAVQVQAGDRPKSIRNLASF 403

RESULT 2

US-08-393-246-8
; Sequence 8, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown

; MOLECULE TYPE: protein
US-08-393-246-8
Query Match 34.9%; Score 687.5; DB 1; Length 405;
Best Local Similarity 38.5%; Pred. No. 3.4e-58;
Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;
QY 15 VCIILGCFMAC--LIYI-----KPTNSWIFSPMESASSVLKMKNEFFSTKTDYFNETTILV 68
Db 28 VCVLAAGLCTALITYACWGLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQTFDL-----TSCQAMFNIOGCHLTDRSLYKNSHAVLIHHRDI-----SW----- 115
Db 69 WWPFGGRDSAPRPPDCPLRNFISGCHLLTDRASYGGAQAVLFHRLDLVKGPPDWPWP 128
QY 116 -----DLTNLPQO-----ARPPFORWIMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDLRLVDYEEAAAAAALATSSPPRPGQWVMNFESPSHGLSLASNL 188
QY 152 FNLTLYRRDSIOVPYGLFVSTNPFVEFVS-----KEKLVGVVWVNNWPEHARV 203
Db 189 FNTLSTRADSDFVPGYLYPRSHP--GDPFSGLAPPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSIEHTYGOAF-GEYVNDKNLPTISACKFYLSFENSIIHKDYITEKLY-NAF 261
Db 247 RYHQLSQHVTVDVFGRGPGQVPVEIGLLHTVARYKFLAFENSQHLDIYITEKLWRL 306
QY 262 LAGSPVVLGSPRENYENIPADSFTHVEDYNSPSELAKYLKVEDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDPRANYERFVRGAFIHDVDFPSASSLASYLFLDRNPVAVYRRYFHWR 366
QY 322 FTVNLPFRWESHACLADHVHQRQY-KSVGNLEKWF 357
Db 367 YAVHTSFDEWPCWCRVQAVQVQAGDRPKSIRNLASF 403
RESULT 3
US-08-525-058A-8
; Sequence 8, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEFAX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-525-058A-8

Query Match 34.9%; Score 687.5; DB 1; Length 405;
Best Local Similarity 38.5%; Pred. No. 3.4e-58;
Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETILV 68
Db 28 VCVLAAAGLTCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQTDL-----TSCQAMFNIOGCHLTDRSLYKSHAVLIHHRDI-----SW----- 115
Db 69 WWPFGGDSAPRPPDCPLRFNISGCRLLTDRASYGEAQAVLFHHRDLVKGPDPDPPW 128
QY 116 -----DLTNLPQO-----ARPPFQKIWMNLESTHTP-OKSGTEHL 151
Db 129 GIQHTAEVDLRLVDYEAAAAEALATSPRPPGQWVMNFESHSGLSLASNL 188
QY 152 FNLTLTYRRSDIQVPYGFGLTVSTNPFVEVPS-----KEKLVGVVSNWNPHEARV 203
Db 189 FNTLSYRADSDVPYGYLYPRSH--GDPPSGLAPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSTEIHTYQAF-GEYVNDKNLPTISACKFYLSFENSIIKDYITEKLY-NAF 261
Db 247 RYHQLSQHVTVDVFGRGQGPVPEIGLLHTVARYFYLAFAFENSQHLDTYTEKLWRNL 306
QY 262 LAGSVPVVLGSPRENYIIPADSFIVEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGDRANYERFVRGAFIHVDFFPSASSLASYLFLDRNPVRYRFFHRRS 366
QY 322 FTVNLPRFWESHACLDHVKRHOEY-KSVGNLEKWF 357
Db 367 YAVHITSEWDEPWCRCVQAVQVORAGDRPKSIRNLASWF 403

RESULT 4

US-08-696-731-8
; Sequence 8, Application US/08696731
; Patent No. 5955347
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,731
; FILING DATE: 14-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281

; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallie, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-696-731-8

Query Match 34.9%; Score 687.5; DB 2; Length 405;
Best Local Similarity 38.5%; Pred. No. 3.4e-58;
Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;

QY 15 VCIILGCFMAC--LLIYI----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETILV 68
Db 28 VCVLAAAGLTCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WWPFGQTDL-----TSCQAMFNIOGCHLTDRSLYKSHAVLIHHRDI-----SW----- 115
Db 69 WWPFGGDSAPRPPDCPLRFNISGCRLLTDRASYGEAQAVLFHHRDLVKGPDPDPPW 128
QY 116 -----DLTNLPQO-----ARPPFQKIWMNLESTHTP-OKSGTEHL 151
Db 129 GIQHTAEVDLRLVDYEAAAAEALATSPRPPGQWVMNFESHSGLSLASNL 188
QY 152 FNLTLTYRRSDIQVPYGFGLTVSTNPFVEVPS-----KEKLVGVVSNWNPHEARV 203
Db 189 FNTLSYRADSDVPYGYLYPRSH--GDPPSGLAPLSRKQGLVAVVSHWDERQARV 246
QY 204 KYNELSKSTEIHTYQAF-GEYVNDKNLPTISACKFYLSFENSIIKDYITEKLY-NAF 261
Db 247 RYHQLSQHVTVDVFGRGQGPVPEIGLLHTVARYFYLAFAFENSQHLDTYTEKLWRNL 306
QY 262 LAGSVPVVLGSPRENYIIPADSFIVEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGDRANYERFVRGAFIHVDFFPSASSLASYLFLDRNPVRYRFFHRRS 366
QY 322 FTVNLPRFWESHACLDHVKRHOEY-KSVGNLEKWF 357
Db 367 YAVHITSEWDEPWCRCVQAVQVORAGDRPKSIRNLASWF 403

RESULT 5

US-09-042-531-8
; Sequence 8, Application US/09042531
; Patent No. 6268193
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/042,531
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA: US/08/393,246
;; APPLICATION NUMBER:
;; FILING DATE:
;; APPLICATION NUMBER: US 08/220,433
;; FILING DATE:
;; APPLICATION NUMBER: US 07/914,281
;; FILING DATE: 20-JUL-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)321-4500
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 405 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-09-042-531-8

Query Match 34.9%; Score 687.5; DB 4; Length 405;
Best Local Similarity 38.5%; Pred. No. 3,4e-58;
Matches 153; Conservative 59; Mismatches 110; Indels 75; Gaps 14;
QY 15 VCIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETILV 68
Db 28 VCVLAAGLCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WYWPFGOTFDL---TSCQAMFIQCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
Db 69 WNEPFGGRDSAPRPDPDCLRENISGCRLLTDRASGCAQVLFHHRDLVKGPDWPPW 128
QY 116 -----DLTNLPQO-----ARPPFOKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDRLVDYEEAAAAEALATSPRPFGQWVMNFPESHSPGLSLASNL 188
QY 152 FNLTLYRRSDIQVPGFLVSTNPFVFEVPS-----KEKLVGVVSNWNPEHARY 203
Db 189 FNTLYSRADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARY 246
QY 204 KYTNELSKSIEIHTYQQAQF-GEYVNDKNLIPTISACKFYLSFENSIIKDYITEKLY-NAF 261
Db 247 RYHQLSQHVTVDFGRGGPGQVPEIGLHTVARYKFLAFENSQHLDTYTEKLWRNAL 306
QY 262 LAGSVPVVLGSPRENYENIIPADSFIVHEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDRAHYERFVRGAFIHVDDFPSASSLASYLFLDRNPVAVRYRHFHWR 366
QY 322 FTVNLPRFWEHSHACLDHVKRHOEY-KSVGNLEKWF 357
Db 367 YAVHITSFWDEPWCRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 6
US-08-483-151-4
; Sequence 4, Application US/08483151
; Patent No. 5858752
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian
; APPLICANT: Holgersson, Jan
; TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street

;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/483,151
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lech, Karen F.
;; REGISTRATION NUMBER: 35,238
;; REFERENCE/DOCKET NUMBER: 00786/278001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200134
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 405 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-483-151-4
Query Match 34.2%; Score 673.5; DB 2; Length 405;
Best Local Similarity 37.8%; Pred. No. 7,6e-57;
Matches 150; Conservative 61; Mismatches 111; Indels 75; Gaps 14;
QY 15 VCIILGCFMAC--LLIYI-----KPTNSWIFSPMESASSVLKMKNFSTKTDYFNETILV 68
Db 28 VCVLAAGLCTALITYACWGQLPLPWA-SPTPS-----RPVGVLL 68
QY 69 WYWPFGOTFDL---TSCQAMFIQCHLTDRSLYNKSHAVLIHHRDI-----SW----- 115
Db 69 WNEPFGGRDSAPRPDPDCLRENISGCRLLTDRASGCAQVLFHHRDLVKGPDWPPW 128
QY 116 -----DLTNLPQO-----ARPPFOKWIWMNLESPTHTP-QKSGIEHL 151
Db 129 GIOAHTAEVDRLVDYEEAAAAEALATSPRPRAKRWYVMNFPESHSPGLSLASNL 188
QY 152 FNLTLYRRSDIQVPGFLVSTNPFVFEVPS-----KEKLVGVVSNWNPEHARY 203
Db 189 FNTLYSRADSDVFPYGYLYPRSHP--GDPPSGLAPPLSRKQGLVAVVSHWDERQARY 246
QY 204 KYTNELSKSIEIHTYQQAQF-GEYVNDKNLIPTISACKFYLSFENSIIKDYITEKLY-NAF 261
Db 247 RYHQLSQHVTVDFGRGGPGQVPEIGLHTVARYKFLAFENSQHLDTYTEKLWRNAL 306
QY 262 LAGSVPVVLGSPRENYENIIPADSFIVHEDYNPSSELAKEYLKEVDKNNKLYLSYFNWRKD 321
Db 307 LAGAVPVVLGPDRAHYERFVRGAFIHVDDFPSASSLASYLFLDRNPVAVRYRHFHWR 366
QY 322 FTVNLPRFWEHSHACLDHVKRHOEY-KSVGNLEKWF 357
Db 367 YAVHITSFWDEPWCRCVQAVQVQAGDRPKSIRNLASWF 403

RESULT 7
PCP-US91-00899-6
; Sequence 6, Application PCP/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: Lowe, John B.
; TITLE OF INVENTION: Method and Products For the Synthesis of
; TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids,
; TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned
; TITLE OF INVENTION: Genetic Sequences That Determine These Structures
; NUMBER OF SEQUENCES: 16

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 Jefferson Davis Highway, Suite 400
;; CITY: Arlington
;; STATE: Virginia
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/00899
;; FILING DATE: 19910214
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye Ph.D., Jean-Paul
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-5940
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 299 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEetical: YES
;; FRAGMENT TYPE: C-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; TISSUE TYPE: Blood
;; CELL LINE: A431
;; PCT-US91-00899-6

Query Match 33.9%; Score 667; DB 5; Length 299;
Best Local Similarity 43.1%; Pred. No. 2e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVWPFQGFDTSCQAMP-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
Db 3 ILLTWPFHPIVALSRCEMVGPGADCHITADRVYPOADTVIVHH-----WDIMSNPKSR 58
QY 120 LPOQARPPFQKWIWNLESPTHTPKSGIEHLNLTLYRRDSDIQVPGFLTV-STNPF 178
Db 59 LPPSPRQGORWIWNLPPNCOHLEALDRYFNLTMSYRSDSDIFTYPGWLWPSGQPA 118
QY 179 --VFEVPSKEKLVGVVSNWNPHEHARVYKYNELSKSIEHTYHGYQAFGEYVNDKNLIPTIS 236
Db 119 HPPLNLSAKTELVAWVSNWKPDSARVRYQSLQAHLKVDVYGRSH-KPLPKGTMMETLS 177
QY 237 ACKVYLSFENSIHKDYITEKLY-NAFLAGSVVVLGSPRENYENYIPADSIHVHEDYNP 295
Db 178 RYKYLAFENSLHPDYITEKLRNALNALEAWVPVWLGPSRSNYERFLPPDAFIHVDQFSP 237
QY 296 SELARKYLEVDKNNKLLSYFNWRKDFTVNLP--FWESHACACLDHVKRHOEYKSVGNL 353
Db 238 KDLARYLQELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLOQESRYQTVERSI 294
QY 354 EKWF 357
Db 295 AAWF 298

RESULT 8
US-07-914-281-2
; Sequence 2, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.

;; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
;; TITLE OF INVENTION: GLYCOPOLYDIP, OR AS FREE MOLECULES, AND FOR THE ISOLATION
;; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/07/914, 281
;; FILING DATE: 19920720
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-4500
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 361 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-07-914-281-2

Query Match 33.9%; Score 667; DB 1; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVWPFQGFDTSCQAMP-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
Db 65 ILLTWPFHPIVALSRCEMVGPGADCHITADRVYPOADTVIVHH-----WDIMSNPKSR 120
QY 120 LPOQARPPFQKWIWNLESPTHTPKSGIEHLNLTLYRRDSDIQVPGFLTV-STNPF 178
Db 121 LPPSPRQGORWIWNLPPNCOHLEALDRYFNLTMSYRSDSDIFTYPGWLWPSGQPA 180
QY 179 --VFEVPSKEKLVGVVSNWNPHEHARVYKYNELSKSIEHTYHGYQAFGEYVNDKNLIPTIS 236
Db 181 HPPLNLSAKTELVAWVSNWKPDSARVRYQSLQAHLKVDVYGRSH-KPLPKGTMMETLS 239
QY 237 ACKVYLSFENSIHKDYITEKLY-NAFLAGSVVVLGSPRENYENYIPADSIHVHEDYNP 295
Db 240 RYKYLAFENSLHPDYITEKLRNALNALEAWVPVWLGPSRSNYERFLPPDAFIHVDQFSP 299
QY 296 SELARKYLEVDKNNKLLSYFNWRKDFTVNLP--FWESHACACLDHVKRHOEYKSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETLR---PRFSWALDFCKACWKLOQESRYQTVERSI 356
QY 354 EKWF 357
Db 357 AAWF 360

RESULT 9
US-08-393-246-2
; Sequence 2, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.

;; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
;; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
;; TITLE OF INVENTION: GLYCOPOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
;; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 Jefferson Davis Highway, Fourth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/393,246
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/220,433
;; FILING DATE: 30-MAR-1994
;; APPLICATION NUMBER: US 07/914,281
;; FILING DATE: 20-JUL-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lavalleye, Jean-Paul M. P.
;; REGISTRATION NUMBER: 31,451
;; REFERENCE/DOCKET NUMBER: 2363-060-55
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)521-4500
;; TELEFAX: (703)486-2347
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 361 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-393-246-2

Query Match 33.9%; Score 667; DB 1; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;

QY 66 ILVWVPFGQTDLTSCQAMF-NIOGCHLTDRSLYKNSHAVLIHHRDISWDL-----TN 119
DB 65 ILLWTWPFHIPVALSRCSEMPGTADCHITADRKVYPOADTVIVHH---WDIMSNPKSR 120
QY 120 LPOQARPPFQKWIMNLESPTHTPQKSGIEHLNLTLYRRSDIOVPYGLTV-STNPF 178
DB 121 LPPSPRQOGRIWNLPPPCQHLADRYFNLTMSYRSDSDIFTFTYGVWLEPWSQPA 180
QY 179 --VFEPVPSKEKLVGVVSNWNPENHARVYKYNELSKSIEHTYQAFGEYVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELVAWVSNWPKDSARVRYQSLOAHKLVYVGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSFENSITHKDYITEKLY-NAFLAGSVVVLGSGSRNENYIPADSFHVEDYNSP 295
DB 240 RYKFYLAENSUHPDYITEKLRNLALEAWVPVVLGSGSRNENYIPADSFHVEDYNSP 299
QY 296 SELAKLYKEVDKNNKLYLSYNWRKDFVNLPR--FWSHACACADHVKKHQEKSYGNL 353
DB 300 KDLARYLQELQKHARYLSYFRWRRTLR---PRFSWALDFCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
DB 357 AAWF 360
RESULT 10

US-08-273-411-3
;; Sequence 3, Application US/08273411
;; Patent No. 5625124
;; GENERAL INFORMATION:
;; APPLICANT: Falk, Per
;; APPLICANT: Gordon, Jeffrey I.
;; TITLE OF INVENTION: Animal Model for Gastro-Intestinal
;; TITLE OF INVENTION: Disease
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Patrea L. Pabst
;; STREET: 1100 Peachtree Street, Suite 2800
;; CITY: Atlanta
;; STATE: Georgia
;; COUNTRY: USA
;; ZIP: 30309-4530
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/273,411
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: WU106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 815-6508
;; TELEFAX: (404) 815-6555
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 361 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: Internal
;; FEATURE:
;; NAME/KEY: misc-feature
;; LOCATION: 1-361
;; OTHER INFORMATION: /note= "GDP-L-fucose:beta-D-N-acetylglucosaminide-3,4-alp
;; PUBLICATION INFORMATION:
;; AUTHORS: Kukowska-Latallo, et al.
;; JOURNAL: Genes & Development
;; VOLUME: 4
;; PAGES: 1288-1303
;; DATE: 1990
;; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 361
US-08-273-411-3

Query Match 33.9%; Score 667; DB 1; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVPFGQTDLTSCQAMF-NIOGCHLTDRSLYKNSHAVLIHHRDISWDL-----TN 119
DB 65 ILLWTWPFHIPVALSRCSEMPGTADCHITADRKVYPOADTVIVHH---WDIMSNPKSR 120
QY 120 LPOQARPPFQKWIMNLESPTHTPQKSGIEHLNLTLYRRSDIOVPYGLTV-STNPF 178
DB 121 LPPSPRQOGRIWNLPPPCQHLADRYFNLTMSYRSDSDIFTFTYGVWLEPWSQPA 180
QY 179 --VFEPVPSKEKLVGVVSNWNPENHARVYKYNELSKSIEHTYQAFGEYVNDKNLIPTIS 236
DB 181 HPPLNLSAKTELVAWVSNWPKDSARVRYQSLOAHKLVYVGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSFENSITHKDYITEKLY-NAFLAGSVVVLGSGSRNENYIPADSFHVEDYNSP 295
|||||:|||||:|||||: || |||:|||||: ||| |||:|||||: |||

Db 240 RYKFLAFENSLHPDYITEKLRNALNAEAVPVVVLGSPRSNYERFLPPDAFIHVDDFQSP 299
QY 296 SELAKYLKEVDKNNKLYLSYFNWRKDFTVNLPR--FWESHACIACADHVRKHQYKSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETILR---PRSFWSALDCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
Db 357 AAWF 360

RESULT 11
US-08-525-058A-2
; Sequence 2, Application US/08525058A
; Patent No. 5770420
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS.
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,058A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-058A-2

Query Match 33.9%; Score 667; DB 1; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVPFGTDFDITSCOAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
Db 65 ILLWTWPFHPVALSRCSSEMPVGTADCHITADRKVYPQADTVIVHH-----WDMNPKSR 120
QY 120 LPQARPPFOKWIWMNLESPTHTPQKSGIEHLENLTLYRRSDIOVPYGLFV-STNPF 178
Db 121 LPSPRPGQGWIFWNLPPPCNQHLEALDRYFNLTMSYRSDSDIPTPYGWLPEWWSQPA 180
QY 179 --VFEVPSKEKLYCWVSNNDPEHARVYKYNELSKSIEHTYQAGFYNDKNLPTIS 236
Db 181 HPLNLSAKTELVAWVSNWPKPSARVYQSLQAHLKVDVYGRSH-KPLPKGTMMETLS 239
QY 237 ACKFYLSFENSIIKDYITEKLY-NAFLAGSVPVVVLGSPRSNYENIYPADSFIVEDYNSP 295
Db 240 RYKFLAFENSLHPDYITEKLRNALNAEAVPVVVLGSPRSNYERFLPPDAFIHVDDFQSP 299

QY 296 SELAKYLKEVDKNNKLYLSYFNWRKDFTVNLPR--FWESHACIACADHVRKHQYKSVGNL 353
Db 300 KDLARYLQELDKDHARYLSYFRWRETILR---PRSFWSALDCKACWKLOQESRYQTVRSI 356
QY 354 EKWF 357
Db 357 AAWF 360
RESULT 12
US-08-696-731-2
; Sequence 2, Application US/08696731
; Patent No. 5955347
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS.
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,731
; FILING DATE: 14-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/393,246
; FILING DATE:
; APPLICATION NUMBER: US 08/220,433
; FILING DATE: 30-MAR-1994
; APPLICATION NUMBER: US 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELETYPE: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-696-731-2
Query Match 33.9%; Score 667; DB 2; Length 361;
Best Local Similarity 43.1%; Pred. No. 2.7e-56;
Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;
QY 66 ILVWVPFGTDFDITSCOAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
Db 65 ILLWTWPFHPVALSRCSSEMPVGTADCHITADRKVYPQADTVIVHH-----WDMNPKSR 120
QY 120 LPQARPPFOKWIWMNLESPTHTPQKSGIEHLENLTLYRRSDIOVPYGLFV-STNPF 178
Db 121 LPSPRPGQGWIFWNLPPPCNQHLEALDRYFNLTMSYRSDSDIPTPYGWLPEWWSQPA 180


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Matches 131; Conservative 55; Mismatches 98; Indels 20; Gaps 9;

Qy 66 ILVWVWPGQTFDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-----TN 119
Db 65 ILLWTWPFHIFVALSRGSEMPVGTADCHITADRVKVPQADTVIVHH-----WDMNSPKSR 120

Qy 120 LPOARPPFQKWIWNLESPTHTPKSGIEHLFNLTLTYRRSDIOVPYGLTV-STNPF 178
Db 121 LPPSRPQGWIMFNLEPPNCHLEALDRYFNLMTSYRSDSDIFTPTGWLSPWGOQA 180

Qy 179 --VEVPSKEKLVCVWVSNWNPENPEHARVYVYNELSKSIEIHTYGOAFGEVYVNDKNLIPTIS 236
Db 181 HPLNLSAKTELVAWAVSNWKPDSARVYVYQSLQAHKVDVYGRSH-KPLPKGTMMETLS 239

Qy 237 ACKYLFSENSIHKDYITEKLY-NAFLAGSVVVLGSPSRENYENIYPADSFHVEDYNSP 295
Db 240 RYKFLAPENSLHPDYITEKLRNNALEAWAVPVVLGSPSRNYERFLPPDAFIHVDQFSP 299

Qy 296 SELAKYLEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLADCHVKKRQEKYSVGNL 353
Db 300 KDLARYLOELDKDHARYLSYFNWRKDFTVNLP--PRSFWSALDFCKACWKLOQESRYQTVRSI 356

Qy 354 EKWF 357
Db 357 AAWF 360

RESULT 15
US-07-914-281-11
; Sequence 11, Application US/07914281
; Patent No. 5324663
; GENERAL INFORMATION:
; APPLICANT: LOWE, JOHN B.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
; TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/914,281
; FILING DATE: 19920720
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-914-281-11
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Query Match 33.9%; Score 667; DB 1; Length 374;
Best Local Similarity 43.7%; Pred. No. 2.8e-56;

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Matches 131; Conservative 58; Mismatches 99; Indels 12; Gaps 8;

Qy 66 ILVWVWPGQTFDLTSCQAMF-NIQGCHLTDRSLYNKSHAVLIHHRDISWDL-TLNLPQQ 123
Db 78 ILLWTWPFHIFVALSRGSEMPVGTADCHITADRVKVPQADTVIVHHDMIMYNSANLPPP 137

Qy 124 ARPPFQKWIWNLESPTHTPKSGIEHLFNLTLTYRRSDIOVPYGLTV-STNPF--VF 180
Db 138 TRPQGWIMFNLEPPNCHLEALDRYFNLMTSYRSDSDIFTPTGWLSPWGOFAHPPL 197

Qy 181 EVPSKEKLVCVWVSNWNPENPEHARVYVYNELSKSIEIHTYGOAFGEVYVNDKNLIPTISACKF 240
Db 198 NLSAKTELVAWAVSNWKPDSARVYVYQSLQAHKVDVYGRSH-KPLPKGTMMETLSRYKF 256

Qy 241 YLSPENSIIHKDYITEKLY-NAFLAGSVVVLGSPSRENYENIYPADSFHVEDYNSPSELA 299
Db 257 YLAFENSLHPDYITEKLRNNALEAWAVPVVLGSPSRNYERFLPPDAFIHVDQFSPKDLA 316

Qy 300 KYLKEVDKNNKLYLSYFNWRKDFTVNLP--FWESHACLADCHVKKRQEKYSVGNLEKWF 357
Db 317 RYLOELDKDHARYLSYFNWRKDFTVNLP--PRSFWSALDFCKACWKLOQESRYQTVRSIAAWF 373

Search completed: October 8, 2002, 18:52:18
Job time : 20 secs
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